

GenCore version 4.5  
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OM protein - protein search, using sw model  
Run on: October 11, 2000, 06:08:11 ; Search time 15.53 seconds  
(without alignments)  
1283.098 Million cell updates/sec

Title: US-09-405-940-1  
Perfect score: 1664  
Sequence: 1 MGTRILCWAALLLGADHTG.....AVLVSAVLMAMVKRKDSRG 314

Scoring table: BICSUM62  
GapP 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_65;\*  
1: Pir1;\*  
2: Pir2;\*  
3: Pir3;\*  
4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1094.5	65.8	307	2 S0716	T-cell receptor beta
2	1048.5	63.0	309	2 S18894	T-cell receptor beta
3	1036.6	62.3	306	2 S25118	T-cell receptor beta
4	944.9	56.7	179	2 C25777	T-cell receptor beta
5	907.5	54.5	177	1 RWFUCY	T-cell receptor beta
6	855.5	51.5	176	2 PL0064	T-cell receptor beta
7	772.5	46.4	178	2 PQ0075	T-cell receptor beta
8	770.0	46.3	177	2 BA4054	T-cell receptor beta
9	763.5	45.9	178	2 PQ0076	T-cell receptor beta
10	750.0	45.1	177	1 RWNVTC	T-cell receptor beta
11	741.7	44.5	173	2 AA4547	T-cell receptor beta
12	741.7	44.5	319	1 RWFB	T-cell receptor beta
13	736.6	44.2	173	1 RWN81C	T-cell receptor beta
14	732.5	44.0	174	2 AA4828	T-cell receptor beta
15	731.5	43.9	173	1 RWSBC	T-cell receptor beta
16	724.7	43.5	173	2 BA46447	T-cell receptor beta
17	724.7	43.5	237	2 A30602	T-cell receptor beta
18	710.0	42.7	173	2 G27579	T-cell receptor beta
19	661.1	39.7	141	2 S03495	T-cell receptor beta
20	653.0	39.2	139	2 S38393	T-cell receptor beta
21	632.5	38.0	135	2 S57582	T-cell receptor PS
22	621.6	37.3	151	2 S24064	T-cell receptor be
23	570.5	34.3	114	2 PT0733	T-cell receptor be
24	570.5	34.3	115	2 S22035	T-cell receptor be
25	526.5	31.5	125	2 BA45806	T-cell receptor be
26	526.5	31.6	269	2 BA46184	T-cell receptor be
27	510.5	30.7	129	2 S57584	T-cell receptor WI
28	476.0	28.6	114	2 PT0734	T-cell receptor be
29	476.0	28.6	115	2 S22038	T-cell receptor be

#### ALIGNMENTS

RESULT	1	903716	T-cell receptor beta chain precursor (F5) - mouse
C;Species:	Mus musculus (house mouse)	C;Date:	18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 05-Nov-1999
C;Accession:	S0316	R;Palmer, M.S.; Bentley, A.; Gould, K.; Townsend, A.R.M.	R;Title: The T cell receptor from an influenza-A specific murine CTL clone.
A;Reference:	S03715; MUID:89202046	A;Accession:	S03716
A;Molecule type:	mRNA	A;Residues:	1-307 <PAL>
A;Cross-references:	EMBL:X14388; PID:944668; PMID:CAA32563.1; PID:944669	C;Keywords:	T-cell receptor
F;1-19/Domain:	signal sequence	#status predicted <SIG>	
F;20-307/Product:	T-cell receptor beta chain #status predicted <MAT>	F;20-307/Product:	

Query	Match	65.8%; Score: 1094.5; DB 2;
Best Matches	Local Similarity 68.6%; W-matches 34; Indels 5; Gaps 2;	Pred. No. 7.6e-78; W-matches 59; Indels 5; Gaps 2;
Matches 214; Conservative		
QY	1 MGTRILCWALCLIGADHTGAGSOTPSKTYERKGKDVELRCDPISGHITALWYROSIGQ	60
Db	1 MAPRLFCVLCFURAEPIAGVQTPIRKVTGQEAETLWCETSGISAVFVYRQTVQ	60
QY	61 GPBEFLIVFGQTGAADDSSGLPNDREFAVRPGSYSTIKIQTQEQQDSSAYLRAQVAAGNS	120
Db	61 GLEFLIVFRNQAPDDSGPKERESQAQMNPQSHTLKTOSTQPQDSAYLCAS-SSRGG	119
Qy	121 YNEQIFGPGRTRLILEDANVFPPEAVFPEVAVFPEVAVFPEVAVFPEVAVFPEVAVFPEV	180
Db	120 HAEQFGPGTRLTVIEDLNRTPKVSLPEPSKAETANOKATVLCLARGFFPDHVLSW	179
QY	181 WNGREHVSQEVSTDEQPLKEQPAINDSRVLSRVSATEQNPRNHRQCQFYGILSE	240
Db	180 WNGKEVHSQCVSTDQAYE -- SNYKCLSLRVRSNTFWNPRIERFCQYQFHGS	235
QY	241 NDENTQDRAKPTQIVSAEWGRADCGTSESYQGVLSATILYEILLGKATLYAVLVA	300
Db	236 EDKWPEGSPPKVQTQNSAEAWGRADGITSASIHQGVLSATILYEILLGKATLYAVLVS	295
RESULT	2	
S18894	T-cell receptor beta chain precursor - human	
C;Species:	Homo sapiens (man)	

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: S18894 R: Hewitt, C.; Lamb, J.R.; Hill, M.; Owen, M.J.; Ohehir, R.O.; Hayball, J.  
 Submitted to the EMBL Data Library, December 1991  
 A:Description : MHC independent clonal cell energy by direct interaction of Staphylococcus  
 A:Reference number: S18893  
 A:Accession: S18894  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-309 <HEW>  
 A:Cross-references: EMBL:X63456; NID:936732; PIDN:CAA45056.1; PID:936733  
 C:Keywords : T-cell receptor

Query Match Score 63.0% Best Local Similarity 68.3% Prod. No. 2.9e-74; Length 309; Matches 215; Conservative 19; Mismatches 70; Indels 11; Gaps 3;

RESULT 4

QY 1 MGTRLLCWAALCLGADHTGAVSQTPSNKVTGKDVRLCDPISGHTALYWYRQLSGQ 60  
 Db 1 MGTRLLCRAFCFLAVGLDVKVTOSSRYLYKRTGEVKVLECVQDMDEHMFWYRQDPGL 60  
 QY 61 GPFELIYFGTGAADDGSLPNDRFAVEPVGSTVSLTKEQGDSAYLRA---GVAA 116  
 Db 61 GLR-LIVFSYDKMMKEKGDIPEPGYSVSREKKERFSLLESASTNQTSMLCASSSTGLPY 119  
 QY 117 GWSSENEQYFGPGRTRLVLEDLKVNFPPEVAVEPSEAEISHTQATLYCQATGFYPDFH 176  
 Db 120 GYI-----FGSSTRUTVVDEDLNKPPEVAVEPSEAEISHTQATLYCQATGFYPDFH 173  
 QY 177 ELSSWWNGKEVHSVGSTDPOPLKEQPALNDSRVCLSSRLRVSATWQNPNRHFRCQVFY 236  
 Db 174 ELSSWWNGKEVHSVGSTDPOPLKEQPALNDSRVCLSSRLRVSATWQNPNRHFRCQVFY 233  
 QY 237 GLSENDEWTQDRAKPYTQIVSEAVERGADCFTSETSYQQGVLSATLTYEILGKATLYV 296  
 Db 234 GLSENDEWTQDRAKPYTQIVSEAVERGADCFTSETSYQQGVLSATLTYEILGKATLYV 293  
 QY 297 LYSALVLMAMYRKD 311  
 Db 294 LYSALVLMAMYRKD 308

RESULT 3

S25118 T-cell receptor beta chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 05-Nov-1999  
 R:Astrup, F.; Kodelja, V.; Kucharzik, T.; Kisch, E.  
 Submitted to the EMBL Data Library, July 1992  
 A:Description : Characterization of idiotype-specific I-Ed-restricted T suppressor lymphocytes  
 A:Reference number: S25117  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-306 <AUS>  
 A:Cross-references: EMBL:X67128; NID:954678; PIDN:CAA47607.1; PID:954679

Query Match Score 62.3% Best Local Similarity 66.0% Prod. No. 2.6e-73; Length 306; Matches 206; Conservative 32; Mismatches 68; Indels 6; Gaps 2;

QY 1 MGTRLLCWAALCLGADHTGAVSQTPSNKVTGKDVRLCDPISGHTALYWYRQLSGQ 60  
 Db 1 MGTRLLCFCVFLVLIANTHDAGVTPPREEEAKGOTIIKCPYSGHNDLFWFRQTKIO 60  
 QY 61 GPFELIYFGTGAADDGSLPNDRFAVEPVGSTVSLTKEQGDSAYLRAAGWSS 120  
 Db 61 GLELLSYFRSKSLMEDGAFDRFKAEMLNSFSTLKIQTEPKDASVYLCASSLD--NS 118

QY 121 YNEQYFGPGRTRLVLEDLKVNFPPEVAVEPSEAEISHTQATLYCQATGFYPDFH 180  
 Db 119 AEIYFGSGSTRLVLEDLNTPPKVSLFEPSEAEISHTQATLYCQATGFYPDFH 178  
 QY 181 WNGKEVHSVGSTDPOPLKEQPALNDSRVCLSSRLRVSATWQNPRHRCQVFYGLSE 240  
 Db 179 WNGKEVHSVGSTDPOPLKEQPALNDSRVCLSSRLRVSATWQNPRHRCQVFYGLSE 234  
 QY 241 NDENTQDRAKPYTQIVSEAVERGADCFTSETSYQQGVLSATLTYEILGKATLYV 300  
 Db 235 EDKWPEGSKXPKVQNISSAVERGADCFTSETSYQQGVLSATLTYEILGKATLYV 294  
 QY 301 LVLMAMVKKRDKS 312  
 Db 295 LVLMAMVKKRDKS 306

RESULT 4

T-cell receptor beta-2 chain C region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 21-Jan-2000  
 R:Tunncliffe, A.; Kefford, R.; Milstein, C.; Forster, A.; Rabbits, T.H.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 5068-5072, 1985  
 A:Title: Sequence and evolution of the human T-cell antigen receptor beta-chain genes  
 A:Reference number: A94053; MUID:85270467  
 A:Accession: C25777  
 A:Cross-references: GB:M12888  
 A:Residues: 1-179 <TUN>  
 A:Gene: GDB:TCRB  
 A:Cross-references: GDB:1204045; OMIM:186930  
 A:Map position: 7q35-7q35  
 A:Introns: 1/1; 136/1; 136/1; 171/3  
 C:Superfamily: immunoglobulin C region; joining, and constant region gene  
 A:Reference number: A94081; MUID:8609476  
 A:Accession: B24687  
 A:Cross-references: GDB:TCRB  
 A:Residues: 1-179 <TOY>  
 C:Genetics:  
 A:Gene: GDB:TCRB  
 A:Cross-references: GDB:1204045; OMIM:186930  
 A:Map position: 7q35-7q35  
 A:Introns: 1/1; 136/1; 136/1; 171/3  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: T-cell receptor  
 F:24-98/Domain: immunoglobulin homology <TMM>

Query Match Score 56.7% Best Local Similarity 100.0% Prod. No. 1.9e-66; Length 179;  
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 136 EDLKNVFPPEVAVEPSEAEISHTQATLYCQATGFYPDFH 195  
 Db 1 EDLKNVFPPEVAVEPSEAEISHTQATLYCQATGFYPDFH 195  
 QY 196 QPLKEQPALNDSRVCLSSRLRVSATWQNPRHRCQVFYGLSE 255  
 Db 61 QPLKEQPALNDSRVCLSSRLRVSATWQNPRHRCQVFYGLSE 255  
 QY 256 VSAAVERGADCFTSETSYQQGVLSATLTYEILGKATLYV 314  
 Db 121 VSAAVERGADCFTSETSYQQGVLSATLTYEILGKATLYV 314

RESULT 5

RWHCY T-cell receptor beta-1 chain C region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 02-Sep-1997  
 C:Accession: B25777; A01133  
 R:Tunncliffe, A.; Kefford, R.; Milstein, C.; Forster, A.; Rabbits, T.H.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 5068-5072, 1985

A;Title: Sequence and evolution of the human T-cell antigen receptor beta-chain genes .  
A;Reference number: A94053; MUID:85270467  
A;Molecule type: DNA  
A;Residues: 1-177 <TUN>  
A;Cross references: GB:ML12887  
R;Xungi, Y.; Yoshihiko, Y.; Leggett, K.; Clark, S.P.; Aleksander, I.; Mak, T.W.  
Nature 308, 145-149, 1984  
A;Title: A human T cell-specific cDNA clone encodes a protein having extensive homology  
A;Reference number: A93324; MUID:84142269  
A;Accession: A02133  
A;Molecule type: mRNA  
A;Residues: 1-177 <YAN>  
A;Cross references: GB:X00437; GB:K01571  
A;Experimental source: clone Y135  
C;Genetics:  
A;Gene: GDB:TCRB  
A;Cross references: GDB:120405; OMIM:18630  
A;Map Position: 7q35-7q35  
A;Introns: 130/1, 136/1; 171/3  
C;Keywords: immunoglobulin C region; immunoglobulin homology  
C;Supramolecular: heterotrimer; receptor; T-cell; transmembrane protein  
F:14-98/Domain: immunoglobulin homology <IMM>  
F:151-173/Domain: transmembrane status predicted <INT>  
F:173-177/Domain: intracellular #status predicted <INT>  
F:31-96/Disulfide bonds: #status predicted  
Query Match 54.5%; Score 907; DB 1; Length 177;  
Best Local Similarity 97.7%; Pred. No. 1.4e-61; Matches 1; Indels 0; Gaps 0;  
Matches 172; Conservative 1; MisMatches 3;  
Db. 136 EDLKNVPPPEVAFSEAIHTOKATLYCLATGYPDHYELSWWNGKEYHSGVSTDP 195  
QY 1 EDLNKVPPEVAFSEAIHTOKATLYCLATGYPDHYELSWWNGKEYHSGVSTDP 60  
Db. 196 QPLKEPALNDSCRLSSRLRVSATWQPNRHHERCQQVFGLSENDWTDRAKPTQI 255  
QY 1 QPLKEPALNDSCRLSSRLRVSATWQPNRHHERCQQVFGLSENDWTDRAKPTQI 120  
Db. 256 VSREAWGRADCGETSQQGVLSATILYLGLGRATLYAVLVSAVLMAVKRD 311  
QY 1 VSREAWGRADCGETSQQGVLSATILYLGLGRATLYAVLVSAVLMAVKRD 176  
Db. 121 VSREAWGRADCGETSQQGVLSATILYLGLGRATLYAVLVSAVLMAVKRD 178

RESULT 6  
PL0064  
T-cell receptor beta chain V-J-C region - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Mar-1993  
C;Accession: PL0064  
R;Burns, F.R.; Li, X.; Shen, N.; Offner, H.; Chou, Y.K.; Vandenberg, A.A.; Heber-Katz, E.  
J. Exp. Med. 169, 27-39, 1989  
A;Title: Both rat and mouse T cell receptors specific for the encephalitogenic determinants being recognized are different.  
A;Reference number: PL0063; MUID:89080488  
A;Accession: PL0064  
A;Molecule type: mRNA  
A;Residues: 1-267 <BUR>  
A;Cross references: EMBL:XI4319  
C;Keywords: heterodimer; T-cell receptor  
F:1-75/Domain: V region #status predicted <VRE>  
F:16-78/Domain: D region #status predicted <DRD>  
F:79-93/Domain: J region #status predicted <JRE>  
F:94-267/Domain: C region #status predicted <CRE>

Query Match 51.5%; Score 856.5; DB 2; Length 267;  
Best Local Similarity 60.6%; Pred. No. 2e-59; Matches 27; MisMatches 59; Indels 25; Gaps 4;  
Matches 171; Conservative 27;  
QY 40 LRCDPISHTALYWRSLQGQPPEFLYFOGTGAADSGLNDRFRAVRRPGSVSTLKIQ 99  
Db. 2 LSCKQNNHHNNMYRODMCHGLRLIHYSYDVNSTEKGDYPNG-----YKVS 48  
QY 100 RTEQSD-----SAYLRAGY - -AAGWSYYNESYFGGTRLTYLEDLKNVFPPEVAVFE 150  
Db. 49 RPSQODFLTLESAPSQTSVYFASSDSNTVEFFGGTRLTYVEDKTKTPPKVSE 108  
QY 151 PSEAETSHHTOKATLYCLATGYPDHYELSWWNGKEYHSGVSTDPQPKLKEQPALNDSCRYC 210  
Db. 109 PSEAATDOKATLYCLARGEFPDHVELSWWNGKEITRNGVSTDPQAKTES --NNTYC 165  
QY 211 LSSRLURVSAWEQNPRNHRFCQVQYGLSENDWTDRAKPTQIVSEAWGRADCGTS 270  
Db. 166 LSSRLURVSAWEQNPRNHRFCQVQFYGLTEDNWSESPKPVQNIQAGAWGRADCGTS 225  
QY 271 ESYQQGVLSATILYLGLGRATLYAVLVSAVLMAVKRD 312  
Db. 226 ASYQQGVLSATILYLGLGRATLYAVLVSAVLMAVKRSS 267

RESULT 7  
PQ0075  
T-cell receptor beta chain (BTB82 c beta 1) - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: PQ0075  
R;Tanaka, A.; Ishiguro, N.; Shinagawa, M.  
Submitted to JIPID, May 1990  
A;Description: Sequence analysis of bovine T-cell receptor beta chain genes.  
A;Reference number: JQ0472  
A;Accession: PQ0075  
A;Molecule type: mRNA  
A;Residues: 1-178 <TA>  
A;Experimental source: T cell  
A;Genes: BTB82 c beta 1  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: receptor  
F:24-98/Domain: immunoglobulin homology <IMM>  
Query Match 46.1%; Score 772.5; DB 2; Length 178;  
Best Local Similarity 82.0%; Pred. No. 4e-53; Matches 15; Mismatches 16; Indels 1; Gaps 1;  
Matches 146; Conservative 15;  
QY 136 EDLKNVFPPEVAFSEAIHTOKATLYCLATGYPDHYELSWWNGKEYHSGVSTDP 195  
Db. 1 DDLSQHPHPKVAVFSEAIHTOKATLYCLATGYPDHYELSWWNGKEYHSGVSTDP 60  
QY 196 QPLKEPALNDSCRLSSRLRVSATWQPNRHHERCQQVFGLSENDWTDRAKPTQI 255  
Db. 61 EPYKEPARDSDCYCLSRVTAFAFWHNRNHRPCQWFHGLTDQDQEEDRAKPTQI 120  
QY 255 IVSAEAWGRADCGETSQQGVLSATILYLGLGRATLYAVLVSAVLMAVKRD 312  
Db. 121 NISAEAWGRADCGETSQQGVLSATILYLGLGRATLYAVLVSAVLMAVKRD 178

RESULT 8  
B49054  
T-cell receptor beta chain C region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: B49054  
R;Thome, A.; Pfraff, E.  
Eur. J. Immunol. 23, 1005-1010, 1993  
A;Title: Molecular cloning of porcine T cell receptor alpha, beta, gamma and delta ch  
A;Reference number: A49054; MUID:9238851  
A;Accession: B49054  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-177 <THO>  
A;Cross-references: GB:L21159; NID:9309198; PID:NAAA6021; PMID:930886  
A;Note: sequence extracted from NCBI backbone (NCBIP:130286)

C; Superfamily: immunoglobulin C region; immunoglobulin homology  
 C; Keywords: T-cell receptor  
 F; 24-98/Domain: immunoglobulin homology <IMM>

Query Match 46.3%; Score 770; DB 2; Length 177;  
 Best Local Similarity 81.4%; Pred. No. 6, 2e-53;  
 Matches 144; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 136 EDLKNVFPPEVAVEPEPSEAISSHTQRATLVCLATGFPDHYELSWVNGKEVHSGYSTDP 195  
 DB 1 DDLQVRPPKVAVEPEPSEAISSHTQRATLVCLATGFPDHYELSWVNGKROYQSGYSTDL 60  
 QY 196 QPIKEQPAINDSYCLSSLRLRSATEFQNPRHFCRQCYQFLSENDEWTQDRAKPVTOI 255  
 DB 61 QPYVEDPSRNDSYCLSSLRLRSATEFQNPRHFCRQCYQFLSENDEWTQDRAKPVTOI 255  
 QY 256 VSAEANGRADCGFTSESSQGVLSATILYEILLGKATLYAVIVSALVLMAMVKRKDS 312  
 DB 121 ISAEAWGRADCFSASSTQGVLSATILYEILLGKATLYAVIVSALVLMATVKKDS 177

RESULT 9  
 P00076 T-cell receptor beta chain (BTB13 c beta 2) - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
 C;Accession: PQ0076  
 R;Tanaka, A.; Ishiguro, N.; Shinagawa, M.  
 A;Description: Sequence analysis of bovine T-cell receptor beta chain genes.  
 Submitted to JPTID, May 1990  
 A;Reference number: J00472  
 A;Accession: PQ0076  
 A;Molecule type: mRNA  
 A;Residues: 1-178 <TAN>  
 A;Experimental source: T cell  
 C;Genetics:  
 A;Gene: BTB13 c beta 2  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: receptor  
 F; 24-98/Domain: immunoglobulin homology <IMM>

Query Match 45.9%; Score 763.5; DB 2; Length 178;  
 Best Local Similarity 80.3%; Pred. No. 2e-52;  
 Matches 143; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

QY 136 EDLKNVFPPEVAVEPEPSEAISSHTQRATLVCLATGFPDHYELSWVNGKEVHSGYSTDP 195  
 DB 1 DDLRVPKVAVEPEPSEAISSHTQRATLVCLATGFPDHYELSWVNGKROYQSGYSTDL 60  
 QY 196 QPIKEQPAINDSYCLSSLRLRSATEFQNPRHFCRQCYQFLSENDEWTQDRAKPVTOI 254  
 DB 61 EPIKEDPARDSYCLSSLRLRSATEFQNPRHFCRQCYQFLSENDEWTQDRAKPVTOI 254  
 QY 255 VSAEANGRADCGFTSESSQGVLSATILYEILLGKATLYAVIVSALVLMAMVKRKDS 312  
 DB 121 ISAEAWGRADCFSASSTQGVLSATILYEILLGKATLYAVIVSALVLMATVKKDS 178

RESULT 10  
 RWATC T-cell receptor beta chain C region homolog (T17T-22) - feline leukemia virus  
 C;Species: feline leukemia virus  
 C;Date: 31-Mar-1989 #sequence\_revision 30-Sep-1993 #text\_change 23-Aug-1997  
 R;Fulton, R.; Forrest, D.; McFarlane, R.; Onions, D.; Neil, J. C.  
 Nature 326, 190-194, 1987  
 A;Reference number: A26600; MUTD:87144638  
 A;Accession: C26600  
 A;Molecule type: DNA  
 A;Residues: 1-177 <FUL>

Query Match 45.1%; Score 750; DB 1; Length 177;  
 Best Local Similarity 80.2%; Pred. No. 2e-51;  
 Matches 142; Conservative 9; Mismatches 26; Indels 0; Gaps 0;  
 QY 136 EDLKNVFPPEVAVEPEPSEAISSHTQRATLVCLATGFPDHYELSWVNGKEVHSGYSTDP 195  
 DB 1 EDLKVSPPKVTVLOPSEAEISRLKATLVCLATGFPDHYELSWVNGKEVHSGYSTDP 60  
 QY 196 QPLKEOPALNDSYCLSSLRLRSATEFWONPRHFCRQCYQDFHGLGKDQDNDYPAAKPVTOI 255  
 DB 61 EPYKEOSGANSSYCLSSLRLRSATEFWHNPNHRFCQYDFHGLGKDQDNDYPAAKPVTOI 120  
 QY 256 VSAEAWGRADCFSASSTQGVLSATILYEILLGKATLYAVIVSALVLMAMVKRKDS 312  
 DB 121 VSADWGRADCFSASSTQGVLSATILYEILLGKATLYAVIVSALVLMATVKKDS 177

RESULT 11  
 A46547 T-cell receptor beta-1 chain C region - shrew mouse  
 C;Species: Mus pahari  
 C;Accession: A46547  
 C;Sequence: Mus\_pahari  
 C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 21-Jan-2000  
 R;Jouvin-Marche, E.; Heller, M.; Rudikoff, S.  
 J. Exp. Med. 161, 2083-2088, 1986  
 A;Title: Gene correction in the evolution of the T cell receptor beta chain.  
 A;Reference number: A46547; MUID:87059557  
 A;Accession: A46547  
 A;Cross-references: GB:M28600  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-173 <JOUS>  
 A;Keywords: T-cell receptor  
 F; 24-94/Domain: immunoglobulin homology <IMM>

Query Match 44.5%; Score 741; DB 2; Length 173;  
 Best Local Similarity 79.7%; Pred. No. 1.e-50;  
 Matches 141; Conservative 13; Mismatches 19; Indels 4; Gaps 1;  
 QY 136 EDLKNVFPPEVAVEPEPSEAISSHTQRATLVCLATGFPDHYELSWVNGKEVHSGYSTDP 195  
 DB 1 EDLKVTPKVSLEPSEAEISRLKATLVCLATGFPDHYELSWVNGKEVHSGYSTDP 195  
 QY 196 QPLKEOPALNDSYCLSSLRLRSATEFWONPRHFCRQCYQDFHGLGKDQDNDYPAAKPVTOI 255  
 DB 61 QAYKE---SNNSYCLSSLRLRSATEFWHNPNHRFCQYDFHGLGKDQDNDYPAAKPVTOI 116  
 QY 256 VSAEAWGRADCFSASSTQGVLSATILYEILLGKATLYAVIVSALVLMAMVKRKDS 312  
 DB 117 ISAEAWGRADCFSASSTQGVLSATILYEILLGKATLYAVIVSALVLMATVKKDS 173

RESULT 12  
 RWBB T-cell receptor beta chain precursor (ANA 11) - rabbit  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Accession: A94052; A94616; A02136  
 C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 16-Aug-1996  
 R;Angiolillo, A.L.; Lamoyi, E.; Bernstein, K.E.; Mage, R.G.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 4498-4503, 1985  
 A;Title: Identification of genes for the constant region of rabbit T-cell receptor be

A; Reference number: A94052; MUID:85242712  
 A; Accession: A94052  
 A; Molecule type: mRNA  
 A; Residues: 1-319 <ANG>  
 R; Mage, R.; submitted to the Protein Sequence Database, April 1987  
 A; Reference number: A9616  
 A; Content: Corrections to residues 79-83 and 104-105  
 A; Accession: A94616  
 A; Molecule type: mRNA  
 C; Residues: 79-83 104-105 <MAG>  
 C; Superfamily: immunoglobulin C region; immunoglobulin homology  
 C; Keywords: glycoprotein; heterotrimer; T-cell receptor; transmembrane protein  
 F; 166-240/Domain: immunoglobulin homology <IMM>  
 F; 292-313/Domain: transmembrane #status predicted <INT>  
 F; 314-318/Domain: intracellular #status predicted <INT>  
 F; 671-682/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 736; DB 1; Length 173;  
 Best Local Similarity 79.1%; Pred. No. 2, 6e-50;  
 Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

Qy 136 EDLKNYFPEAYFPESEAISHTOKATLYCLATGFYDPEIVELSKWVNGKEVHSGVSTDP 195  
 Db 1 EDLKNYFPEAYFPESEAISHTOKATLYCLATGFYDPEIVELSKWVNGKEVHSGVSTDP 60

Query Match Score 736; DB 1; Length 173;  
 Best Local Similarity 79.1%; Pred. No. 2, 6e-50;  
 Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

Qy 196 QPLKEQPALNDSCRYCLSRLRVSATFWQNPNNHFRCQVQFYGLSENDEWTQDRAKPTQI 255  
 Db 61 QAYKE --- SNYSYCSLSRLRVSATFWHNRNHFCCQVQFHGLSDEKPEGSPPPTQN 116

Query Match Score 736; DB 1; Length 173;  
 Best Local Similarity 79.1%; Pred. No. 2, 6e-50;  
 Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

Qy 256 VSAEANGRADCGFTSHSYQQGVLSATILYELIGRATLYAVLVSALVLMAMVKRKS 312  
 Db 117 ISAEANGRADCGITSAQQGVLSATILYELIGRATLYAVLVSALVLMAMVKRNS 173

RESULT 14

RBSLT PQLKEQPALNDSCRYCLSRLRVSATFWQNPNNHFRCQVQFYGLSENDEWTQDR A 249  
 Db 197 GVSTDPOQKXQDKSDHEKYCLSSRLRVSAWKHNPNHFRCQVQFYGLDDENTYNS 256

Query Match Score 736; DB 1; Length 173;  
 Best Local Similarity 79.1%; Pred. No. 2, 6e-50;  
 Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

Qy 250 KPVQTQVSAEAWGRADCSETSESYQQGVLSATILYELIGRATLYAVLVSALVLMAMVKR 309  
 Db 257 KPTQNTIAHTRGRADCITSASYYQQGVLSATILYELIGRATLYAVLVSALVLMAMVKR 316

Query Match Score 736; DB 1; Length 173;  
 Best Local Similarity 79.1%; Pred. No. 2, 6e-50;  
 Matches 140; Conservative 16; Mismatches 17; Indels 4; Gaps 1;

Qy 310 KDS 312  
 Db 317 KDS 319

RESULT 13

PWMSLC T-cell receptor beta-1 chain C region - mouse  
 C; Species: Mus musculus (house mouse)  
 Date: 28-Feb-1986 #sequence\_revision 28-Feb-1986 #text\_change 16-Aug-1996  
 R; Gascoline, N.R.J.; Chien, Y.; Becker, D.M.; Kavalier, J.; Davis, M.M.  
 Nature 310, 387-391, 1984  
 A; Title: Genomic organization and sequence of T-cell receptor beta-chain constant- and variable domains  
 A; Reference number: A93336; MUID:8427074  
 A; Accession: B93336  
 A; Molecule type: DNA  
 A; Residues: 1-173 <GAS>  
 A; Cross-references: GB:M26053  
 A; Experimental source: strain B10 A, cytotoxic T lymphocyte  
 R; Hedrick, S.M.; Nielsen, E.A.; Kavalier, J.; Cohen, D.I.; Davis, M.M.  
 Nature 308, 153-158, 1984  
 A; Title: Sequence relationships between T-cell receptor polypeptides and immunoglobulins  
 A; Reference number: A93325; MUID:8414271  
 A; Accession: A93325  
 A; Molecule type: mRNA  
 A; Residues: 1-69, H, 71-173 <HED>  
 A; Cross-references: GB:K01080  
 A; Experimental source: clone 86T1  
 A; Note: the authors translated the codon TAT for residue 134 as Val  
 R; Morinaga, T.; Fotedar, A.; Singh, B.; Wiesmann, T.G.; Tamaki, T.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 8163-8167, 1985  
 A; Title: Isolation of cDNA clones encoding a T-cell receptor beta-chain from a beef insulinoma cell line  
 A; Reference number: A94078; MUID:8606802  
 A; Accession: A23572  
 A; Molecule type: mRNA  
 A; Residues: 1-173 <MCR>  
 A; Cross-references: GB:M11456  
 C; Species: Mus musculus (house mouse)

RESULT 15

RWSBC T-cell receptor beta-2 chain C region - mouse  
 C; Species: Mus musculus (house mouse)

C; Date: 03-Aug-1984 # sequence-revision 28-Feb-1986 #text\_change 05-Sep-1997  
 C; Accession: A93336; B93333; A02134  
 R; Gascoigne, N.R.J.; Chien, Y.; Becker, D.M.; Kavalali, J.; Davis, M.M.  
 A; Title: Genomic organization and sequence of T-cell receptor beta-chain constant- and j  
 A; Reference number: A93336; MUID:84270704  
 A; Accession: A93336  
 A; Molecule type: DNA  
 A; Residues: 1-173 <GA>  
 A; Experimental source: strain B10.A, cytotoxic T lymphocyte  
 R; Saito, H.; Kranz, D.M.; Takagaki, Y.; Hayday, A.C.; Eisen, H.N.; Tonegawa, S.  
 Nature 309, 757-762, 1984  
 A; Title: Complete primary structure of a heterodimeric T-cell receptor deduced from cDNA  
 A; Reference number: A93333; MUID:84245824  
 A; Accession: B93333  
 A; Molecule type: mRNA  
 A; Residues: 1-49, 'R', 51-69, 'H', 71-173 <SA>  
 A; Experimental source: BALB.B, clone 2C, cytotoxic T lymphocyte  
 C; Genetics:  
 A; Introns: 1/1; 126/1; 132/1; 163/3  
 C; Superfamily: immunoglobulin C region; immunoglobulin homology  
 C; Keywords: glycoprotein; heterotrimer; receptor; T-cell; transmembrane protein  
 F; 24-94 /Domain: immunoglobulin homology <IMM>  
 F; 147-168 /Domain: immunoglobulin homology <IMM>  
 F; 169-173 /Domain: transmembrane domain: status predicted <NT>  
 F; 67-116 /Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.9% Score 731; DB 1; Length 173;  
 Best Local Similarity 78.5%; Pred. No. 6.4e-50;  
 Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;  
 Qy 136 EDLKNVFPPEVAYPEPSEAFIHSHTOKATLVCLATGEPDPHVELSWWNGKEVHSGYSTDP 195  
 Db 1 EDLERNVTPEPKVSLFPEPSKAEIAINKOKATLVCLARGEFPDPHVELSWWNGKEVHSGYSTDP 60  
 Qy 196 QPKEQPALNDSRYKLSSRLRVSATFMNPRHFRQVOFTYGLSENDEWTQDRAKPTQI 255  
 Db 61 QAYKE----SNSYCYCLSSRLRVSATFWHNPRHFRQVOFHLSEDDKWPEGSPKVTON 116  
 Qy 256 VSAAWGRADCGTSESYQGVLSATILYEILIGKATLYAVLVSALVLMAVKRKDS 312  
 Db 117 ISAAFWGRADCGTISASYHQGVLSATILEILIGKATLYAVLVSGLVLMAMVKKNS 173

Search completed: October 11, 2000, 06:09:02  
 Job time: 51 sec



SEQUENCE FROM N.A.	
RP MEDLINE: 85247212.	RA Angiolillo A.L., Lamoyi E., Bernstein K.E., Mage R.G., Mage R.G., "Identification of genes for the constant region of rabbit T-cell receptor beta chains"; Proc. Natl. Acad. Sci. U.S.A. 82:4498-4502(1985).
RT [2]	RP REVISIONS TO 79-83 AND 104-105.
RL DR PIR: A02136; PWRRBB.	RA Mage R.G.; DR PIR: A02136; PWRRBB.
RN [2]	DR PFAM; PF00047; ig; 1.
FT DOMAIN; 142 273 C REGION.	KW T-cell; Receptor; transmembrane; Glycoprotein.
FT TRANSMEM 292 313	FT DOMAIN 314 319 CYTOPLASMIC TAIL.
FT CARBOHYD 147 147	FT CARBOHYD 164 164 POTENTIAL.
FT CARBOHYD 254 254	FT CARBOHYD 262 262 POTENTIAL.
SQ 319 AA; 36068 MW; AAB2C305ED45306 CRC64;	SQ 319 AA; 36068 MW; AAB2C305ED45306 CRC64;
Query Match 44.5%; Score 741; DB 1; Length 319; Best Local Similarity 76.5%; Pred. No. 2.e-55; Mismatches 17; Indels 0; Gaps 0;	Query Match 44.5%; Score 741; DB 1; Length 319; Best Local Similarity 76.5%; Pred. No. 2.e-55; Mismatches 17; Indels 0; Gaps 0;
Matches 140; Conservative 17; Mismatches 26; Indels 0; Gaps 0;	Matches 140; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 130 TRIVLEDKNVPPEVAFEPSEAEISITQATLVCLATGFYPPDHVELSWWWNGKEVHS 189	QY 130 TRIVLEDKNVPPEVAFEPSEAEISITQATLVCLATGFYPPDHVELSWWWNGKEVHS 189
Db 137 TPLHFPEDLANSVAPQVYEDPSEAEINTQATLVCLADKFYDPHVLSWWNGKEVHN 196	Db 137 TPLHFPEDLANSVAPQVYEDPSEAEINTQATLVCLADKFYDPHVLSWWNGKEVHN 196
QY 190 GVSTDPPQLREQPALNDSSRYLSATEFQNPRNHRFCRQFYGLSENDEWTQDR 249	QY 190 GVSTDPPQLREQPALNDSSRYLSATEFQNPRNHRFCRQFYGLSENDEWTQDR 249
Db 197 GVSTDPPKQDPKDSHSSYCLSSRLRVSAAFWHPNPRNHRFCRQFYGLIDDEWTYNS 256	Db 197 GVSTDPPKQDPKDSHSSYCLSSRLRVSAAFWHPNPRNHRFCRQFYGLIDDEWTYNS 256
QY 250 KPVTOIVSAEAWGRADCGFTSETSQGVLSATILYEILLGKATLYVALVLMAMYKR 309	QY 250 KPVTOIVSAEAWGRADCGFTSETSQGVLSATILYEILLGKATLYVALVLMAMYKR 309
Db 257 KPTQNISAHTRGRADCGFSSASTQQGVLSATVLYEILLGKATLYVALVLMAMYVR 316	Db 257 KPTQNISAHTRGRADCGFSSASTQQGVLSATVLYEILLGKATLYVALVLMAMYVR 316
QY 310 KDS 312	QY 310 KDS 312
Db 317 KDS 319	Db 317 KDS 319
RESULT 4	RESULT 4
TCB1_MOUSE STANDARD; PRT; 173 AA.	TCB1_MOUSE STANDARD; PRT; 173 AA.
ID _TCB1_MOUSE P01552; AC P01552;	ID _TCB1_MOUSE P01552;
DT 21-JUL-1986 (Rel. 01, Created)	DT 21-JUL-1986 (Rel. 01, Last sequence update)
DB 1 EDLARVFPPEVAFEPSEAEISITQATLVCLATGFYPPDHVELSWWWNGKEVHS 195	DB 1 EDLARVFPPEVAFEPSEAEISITQATLVCLATGFYPPDHVELSWWWNGKEVHS 195
QY 196 QPKEQPALNDSSRYLSATEFQNPRNHRFCRQFYGLSENDEWTQAKPTQI 255	QY 196 QPKEQPALNDSSRYLSATEFQNPRNHRFCRQFYGLSENDEWTQAKPTQI 255
Db 61 QPKEQPALNDSSRYLSATEFQNPRNHRFCRQFYGLSENDEWTQAKPTQI 120	Db 61 QPKEQPALNDSSRYLSATEFQNPRNHRFCRQFYGLSENDEWTQAKPTQI 120
QY 256 VSAAWGRADCGFTSETSQGVLSATILYEILLGKATLYVALVLMAMYRK 311	QY 256 VSAAWGRADCGFTSETSQGVLSATILYEILLGKATLYVALVLMAMYRK 311
Db 121 VSAAWGRADCGFTSVSQGVLSATILYEILLGKATLYVALVLMAMYRK 176	Db 121 VSAAWGRADCGFTSVSQGVLSATILYEILLGKATLYVALVLMAMYRK 176
RESULT 3	RESULT 3
TCB1_RABBIT STANDARD; PRT; 319 AA.	TCB1_RABBIT STANDARD; PRT; 319 AA.
AC P06333; DT 01-JAN-1988 (Rel. 06, Created)	AC P06333; DT 01-JAN-1988 (Rel. 06, Last sequence update)
DB 15-FEB-2000 (Rel. 39, Last annotation update)	DB 15-FEB-2000 (Rel. 39, Last annotation update)
OS Oryctolagus cuniculus (Rabbit).	OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus .
RN [1]	RN [1]
RP SEQUENCE FROM N.A. (CLONE 86T1).	RP SEQUENCE FROM N.A. (CLONE 86T1).
RC STRAIN=B10-A; MEDLINE: 8414271.	RC STRAIN=B10-A; MEDLINE: 8414271.
RT "Sequence relationships between putative T-cell receptor polypeptides and immunoglobulins." RT Nature 308:155-158(1984).	RT "Sequence relationships between putative T-cell receptor polypeptides and immunoglobulins." RT Nature 308:155-158(1984).
RL -1 MISCELLANEOUS: REF.2 AUTHORS TRANSLATED THE CODON TAT FOR RESIDUE 134 AS VAL.	RL -1 MISCELLANEOUS: CLONE B10-A WAS ISOLATED FROM A CYTOTOXIC T
CC CC	CC CC

-	-	LYMPHOCYTE.	Query Match Score: 43.9%; DB 1; Length 173;
CC	-	MISCELLANEOUS: CLONE 86T1 WAS ISOLATED FROM A CYTOTOXIC T LYMPHOCYTE.	Best Local Similarity 78.5%; Pred. No. 9.4e-55;
CC	PIR; A02135; RMNS1C.	Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;	Matches 139; Conservative 16; Mismatches 18; Indels 4; Gaps 1;
CC	PFAM; PF00047; 19; 1.		
CC	T-cell; Receptor; Transmembrane; Glycoprotein.		
CC	NON_TER 1 1 C REGION.		
CC	DOMAIN 1 146 DOMAIN.		
CC	TRANSMEM 146 167 POTENTIAL.		
CC	DOMAIN 168 173 CYTOPLASMIC TAIL.		
CC	VARIANT 70 70 Y -> H (IN CLONE 86T1).		
CC	SEQUENCE 173 AA: 19346 MW: F9BA735E6D3EAD7 CRC64;		
CC	RESULT 6		
CC	TVB2_HUMAN STANDARD;	PRT; 133 AA.	
CC	ID TVB2_HUMAN		
CC	AC P04435;		
CC	DT 13-AUG-1987 (Rel. 05, Created)		
CC	DE 15-JUL-1999 (Rel. 38, Last annotation update)		
CC	GN TCDB.		
CC	OS Homo sapiens (Human).		
CC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
CC	RN [1]		
CC	RP SEQUENCE FROM N.A.		
CC	RX MEDLINE; 86276770.		
CC	RA Leiden J.M.; Fraser J.D.; Strominger J.L.;		
CC	RT "The complete primary structure of the T-cell receptor genes from an alloreactive cytotoxic human T-lymphocyte clone."		
CC	RT RL Immunogenetics 24:17-23 (1986).		
CC	- - MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A HUMAN CYTOTOXIC T-LYMPHOCYTE THAT IS T3+, T4+, T8. .		
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
CC	CC DR EMBL; M15564; AAA61027.1; -.		
CC	DR PIR; A02001; RWI07B.		
CC	DR PF00047; ig_1.		
CC	KW T-cell; Receptor; Glycoprotein; Signal.		
CC	FT SIGNAL 1 21		
CC	FT CHAIN 22 133 T-CELL RECEPTOR BETA CHAIN V REGION CTL-1.17.		
CC	FT DOMAIN 22 114 V SEGMENT.		
CC	FT DOMAIN 115 118 D SEGMENT.		
CC	FT DOMAIN 119 133 J SEGMENT.		
CC	FT CARBOHYD 30 30		
CC	FT CARBOHYD 37 37		
CC	FT DISULFID 42 111		
CC	FT NON_TER 133 133 14999 MW; 21030818D18D341F CRC64;		
CC	SQ SEQUENCE		
CC	Query Match Score: 26.0%; DB 1; Length 133;		
CC	Best Local Similarity 62.2%; Pred. No. 7.9e-30;		
CC	Matches 84; Conservative 15; Mismatches 34; Indels 2; Gaps 1;		
CC	PIR; A02134; RMNSBC.		
CC	PFAM; PF00047; 19; 1.		
CC	T-cell; Receptor; Transmembrane; Glycoprotein.		
CC	NON_TER 1 1 C REGION.		
CC	DOMAIN 1 146 DOMAIN.		
CC	TRANSMEM 147 168 CYTOPLASMIC TAIL.		
CC	DOMAIN 169 173 K -> R (IN CLONE 2C).		
CC	VARIANT 50 50 Y -> H (IN CLONE 2C).		
CC	VARIANT 70 70 19297 MW; A54581(496)4CF295 CRC64;		
CC	SEQUENCE 173 AA: 19297 MW; A54581(496)4CF295 CRC64;		
CC	DR PIR; A02134; RMNSBC.		
CC	PFAM; PF00047; 19; 1.		
CC	T-cell; Receptor; Transmembrane; Glycoprotein.		
CC	NON_TER 1 1 C REGION.		
CC	DOMAIN 1 146 DOMAIN.		
CC	TRANSMEM 147 168 CYTOPLASMIC TAIL.		
CC	DOMAIN 169 173 K -> R (IN CLONE 2C).		
CC	VARIANT 50 50 Y -> H (IN CLONE 2C).		
CC	VARIANT 70 70 19297 MW; A54581(496)4CF295 CRC64;		
CC	SEQUENCE 173 AA: 19297 MW; A54581(496)4CF295 CRC64;		

QY	61	GPEELIYFOGTGAAADDSSLNPDRFAVPEGSYSTKIORTEQGDSAAYLRAGYAAGWSS	120	SEQUENCE FROM N.A.
Db	61	GPPEFLTYFQEAAQLEKSRRLSDFRFAERPKGSFSTLEIQRTTEQGDSAMYLCASSLAGLN-	119	RX MEDLINE; 8414269.
QY	121	YNOQYFGPGTRITVL	135	RA Yangi, Y., Yoshikai Y., Leggett K., Clark S.P., Aleksander I., Mak T.W.; RA A human T cell-specific cDNA clone encodes a protein having extensive homology to immunoglobulin chains.;
Db	120	-QQHFGDGTTRISIL	133	RT Nature, 308:145-149 (1984).
RESULT	7			RL
TVB7_MOUSE				DR PIR: A02000; RWHUV.
ID	TVB7_MOUSE	STANDARD;	PRT;	DR HSSP; P01789; 2MCP.
AC	P0320;			PFAM; PF00047; ig; 1.
DT	01-JAN-1988	(Rel. 06, Created)		KW T-cell; Receptor; signal.
DT	01-JAN-1988	(Rel. 06, Last sequence update)		FT SIGNAL ?
DT	15-JUL-1999	(Rel. 38, Last annotation update)		FT CHAIN ?
DE	T-CELL RECEPTOR BETA CHAIN V REGION CTL F3 PRECURSOR.			POTENTIAL. T-CELL RECEPTOR BETA CHAIN V REGION YT35.
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 87053852.			
RA	Chou H.S., Behlik M.A.; Godambe S.A., Russell J.H., Brooks C.G., Loh D.Y.;			
RT	"T cell receptor genes in an alloreactive CTL clone: implications for rearrangement and germline diversity of variable gene segments.";			
EMBO J.	5:2149-2155(1986).			
PIR	A02002; RWMSB3.			
DR	PFAM; PF00047; ig; 1.			
KW	T-cell; Receptor; Glycoprotein; Signal.			
FT	SIGNAL	1	1	
FT	CHAIN	19	135	
FT	DOMAIN	20	134	T-CELL RECEPTOR BETA CHAIN V REGION CTL-
FT				F3.
FT	DOMAIN	20	115	V SEGMENT.
FT	DOMAIN	116	119	D SEGMENT.
FT	DOMAIN	120	134	J SEGMENT.
FT	DISLFID	42	111	BY SIMILARITY.
FT	CARBOHYD	90	90	POTENTIAL.
FT	NON_TER	134	134	
SEQUENCE	134 AA;	14946 MW;	C080FB24C81988FF6 CRC64;	
FT	CHAIN	20	134	
FT				
FT	DOMAIN	20	115	
FT	DOMAIN	116	119	
FT	DOMAIN	120	134	
FT	DISLFID	42	111	
FT	CARBOHYD	90	90	
FT	NON_TER	134	134	
SEQUENCE	134 AA;	14946 MW;	C080FB24C81988FF6 CRC64;	
Query Match	22.18.	Score 367.5;	DB 1;	RESULT 9
Best Local Similarity	57.0%	Pred. No. 2.6e-24;		TVB1_MOUSE
Matches	77;	Conservative	15;	ID TVB1_MOUSE
		Mismatches	42;	STANDARD;
		Indels	1;	PRT;
		Gaps	1;	135 AA.
QY	1	MGTRLLCWAALLGADHTGAVSQTPSNKVTEKGRDVEILRCDPISGHATALYWYRQLGQ	60	SEQUENCE FROM N.A.
Db	1	MGPRFLCLVFLPFLRKEPTVQVTPKRYQTKQEAUTWCEPFGSHASAVWFRQTIV	60	RX MEDLINE; 85176939.
QY	61	GPEELIYFOGTGAAADDSSLNPDRFAVPEGSYSTKIORTEQGDSAAYLRAGYAAGWSS	120	RA Goverman J., Minard K., Shastrri N., Hunkapiller T., Hansburg D., Sercarz E., Hood L.;
Db	61	GIEELFLYFRNQPIDSGMPKERSQAMPNQSHSITKIQSTQPSAVYLCASSLSTGV	120	RT Rearranged beta T cell receptor genes in a helper T cell clone specific for Lysozyme: no correlation between v beta and MHC restriction.;
QY	121	YNEQY--TGPGTTRITVL	135	RT Cell 0:859-867 (1985).
Db	121	Y-EQYFGPGTRITVL	134	CC -! MISCELLANEOUS: THIS T-CELL CLONE EXPRESSES ONLY A SINGLE V-BETA CHAIN SEGMENT ALTHOUGH IT HAS THREE REARRANGEMENTS IN THE BETA CHAIN FAMILY.
RESULT	8			CC -! MISCELLANEOUS: THIS REARRANGED V-BETA CHAIN SEGMENT, SPECIFIC FOR CHICKEN EGG-WHITE LYSOZYME AND I-A(B), IS THE SAME AS THAT EXPRESSED IN A T HELPER CELL SPECIFIC FOR CYTOCHROME C AND AN I-E(K) MHC MOLECULE.
TVB1_HUMAN		STANDARD;	PRT;	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
ID	TVB1_HUMAN		135 AA.	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
AC	P01733;	(Rel. 01, Created)		CC the European Bioinformatics Institute. There are no restrictions on its
DT	21-JUL-1986	(Rel. 01, Last sequence update)		CC use by non-profit institutions as long as its content is in no way
DT	21-JUL-1986	(Rel. 01, Last annotation update)		CC modified and this statement is not removed. Usage by and for commercial
DT	15-JUL-1999	(Rel. 38, Last annotation update)		CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> ) or send an email to license@isb-sib.ch).
DE	T-CELL RECEPTOR BETA CHAIN V REGION YT35 PRECURSOR.			CC
OS	Homo sapiens (Human)			CC
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			CC
RN	[1]			CC

T-cell; Receptor; Signal.	1	20	T-CELL RECEPTOR BETA CHAIN V REGION	QY	133	TVL 135
CHAIN	21	- 135	3H.25.			
DOMAIN	21	115	V SEGMENT.			
DOMAIN	116	118	D SEGMENT.			
DOMAIN	119	135	J SEGMENT.			
DISULFID	111	135	BY SIMILARITY.			
NON-TER	135	135	MW: COFFIDACF37E76D CRC64;			
SEQUENCE	135 AA;	15123 MW;				
RESULT 11						
ID TVB4_MOUSE			STANDARD;	PRT;	136	AA.
AC P04212;						
DT 20-MAR-1987 (Rel. 04, Created)						
DT 20-MAR-1987 (Rel. 04, Last sequence update)						
DT 15-JUL-1999 (Rel. 38, Last annotation update)						
DE T-CELL RECEPTOR BETA CHAIN V REGION LB2 PRECURSOR.						
OS Mus musculus (Mouse).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
RN [1]						
RP SEQUENCE FROM N.A.						
RX MEDLINE; 85036636.						
RA Patten P.; Yokota T.; Rothbard J.; Chien Y.; Arai K.; Davis M.M.; RT "Structure, expression and divergence of T-cell receptor beta-chain variable regions."						
RL Nature 312:40-46(1984).						
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A T-HELPER CLONE.						
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DR EMBL: X01643; CAA258001;						
DR PIR: A02007; RWMSLB.						
DR PFAM: PF00047; ig_1.						
CC -----						
FT SIGNAL; Receiver; signal.						
FT DOMAIN	1	21	T-CELL RECEPTOR BETA CHAIN V REGION LB2.			
FT DOMAIN	22	136	V SEGMENT.			
FT DOMAIN	117	120	D SEGMENT.			
FT DISULFID	121	136	J SEGMENT.			
FT NON-TER	45	113	BY SIMILARITY.			
SQ SEQUENCE	136 AA;	15369 MW;	F74DOC0414088D02 CRC64;			
Query Match 10.8%; Score 180.5; DB 1; Length 136;						
Best Local Similarity 32.6%; Pred. No. 1.4e-08;						
Matches 45; Conservative 25; Mismatches 63; Indels 5; Gaps 3;						
QY 1 MGPRLLCWAALCLGADHT--GAGVSQTPSNKVTEKGKDVLRCDPTSGHTALWYROS 57						
DR 1 MNKPKVCTLCLLTVETHGDDIIITQPKLIGQESKLTIKCQNEENHDMMWYQD 60						
QY 58 LGQCPPEFLIYFOQTGAADSPGLNDRFAVPGSVSTKLQRIQEQQDSAAYLRYAVG 117						
DR 61 SGRLR-LIYYSSTENDLQKDLSSEGYDASREKKSSFSUTVTSQAKNEMTVELCAS-SIR 118						
QY 118 WSSYNEQYFGPSTRLVYL 135						
Query Match 11.0%; Score 183; DB 1; Length 122;						
Best Local Similarity 35.8%; Pred. No. 7.7e-09;						
Matches 44; Conservative 16; Mismatches 61; Indels 2; Gaps 2;						
RESULT 12						
ID LAC2_RAT			STANDARD;	PRT;	104	AA.
AC P20167;						
DT 01-FEB-1991 (Rel. 17, Created)						
DT 01-FEB-1991 (Rel. 17, Last sequence update)						
DT 01-JUL-1999 (Rel. 38, Last annotation update)						
DE IG_LAMBDA-2_CHAIN_C_REGION.						
QY 13 IJGADHTGAGVSQTPSNKVTEKGKDVLRCDPTSGHTALWYROS1GQGPFLIYFOGTG 72						
DR 2 LIQAKHEAVTQSPRSAYVQGKVTLSCHTNNHYMWQRDTHGLRJLHYSYVAD 61						
QY 73 ADDSGLPNDRFPVPRPGSVSTKLQRIEQGDSAAYLRYAVGSSYNEYFGPTRL 132						
DR 62 STEKGDT-DGXKAQSPRSOENFELASLSCATAYFCASSGT-GALDQTYFGPTRL 119						
SQ SEQUENCE 122 AA; 13349 MW; D657DC9B261C64C CRC64;						

CS	Rattus norvegicus (Rat).	SQ	SEQUENCE	133 AA;	14986 MW;	73DE9EBF6F85290 CRC64;
CC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RY	MEDLINE; 87305594.					
RA	Stein M.L., Peltersson U.;	Query	Match 9.9%;	Score 165;	DB 1;	Length 133;
RT	"The immunoglobulin lambda locus in rat consists of two C lambda	Best Local Similarity 31.1%;	Pred. No. 2.8e-07;			
RT	genes and a single V lambda gene.";	Matches 42;	Conservative 22;	Mismatches 69;	Indels 2;	Gaps 2;
RC	Gene 55:75-84(1987).					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	Qy 1 MGTRLLCWAALCLIGADHTGAGVSQTPSNKVTEKGKDVELRCDPISGHTALYWYROSGLQ 60				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	Db 1 MSCRLILYSLCLVETALMNTKTTQSPrVLGRA-NKSLECEQHLGHAMMYWQSAEK 59				
CC	the European Bioinformatics Institute. There are no restrictions on its	Qy 61 GPEFLIYFGQGIAADDGLPNDRFAVPRPGSVSTLKRTEQDSDAANLRAVAGNWS 120				
CC	use by non-profit institutions as long as its content is in no way	Db 60 PPELMFLYNLKOLIRNETVPS-RFIEPECDSKULLHISAVDPEDSAVYFCASSHGQGVs 118				
CC	modified and this statement is not removed. Usage by and for commercial	Qy 121 YNEQYFGGPGRTRLV 135				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	Db 119 GNTLYFGEGSPLIVV 133				
CC	or send an email to license@isb-sib.ch).					
DR	EMBL; M2521; AAA41420.1; ALT_INIT.					
DR	PIR; B27390; B27390.	RESULT 14				
DR	PFAM; PF00047; ig_1.	ID TVB8_MOUSE STANDARD; PRT: 130 AA.				
DR	PROSITE; PS00290; IG_MHC; 1.	AC P06321;				
KW	Immunoglobulin domain; Immunoglobulin C region.	DT 01-JAN-1988 (Rel. 06; Created)				
FT	NON_TER 1	DT 01-JAN-1988 (Rel. 06; Last sequence update)				
FT	DISULFID 27	DT 15-JUL-1999 (Rel. 38; Last annotation update)				
FT	DISULFID 85	DE T-CELL RECEPTOR BETA CHAIN V REGION A20.2.25 PRECURSOR.				
FT	SEQUENCE 103	OS Mus musculus (Mouse).				
FT	INTERCHAIN (WITH HEAVY CHAIN).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
FT	SEQUENCE 104 AA; F087906DE45F7276 CRC64;	OC Mammalia; Eutheria; Rodentia; Sciurognathii; Murinae; Mus.				
FT		[1]				
FT		RN FROM N.A.				
FT		RP SEQUENCE FROM N.A.				
FT		RX MEDLINE; 86068062.				
FT		RA MORinaga T., Fotedar A., Singh B., Wegmann T.G., Tamooki T.;				
FT		RT "Isolation of cDNA clones encoding a T-cell receptor beta-chain from a beef insulin-specific hybridoma";				
FT		RL Proc. Natl. Acad. Sci. U.S.A. 82:8163-8167(1985).				
FT		DR PIR; A02005; RWMS20.				
FT		DR PFAM; PF00047; ig_1.				
FT		KW T-cell; Receptor; Glycoprotein; Signal.				
FT		FT SIGNAL 21 BY SIMILARITY.				
FT		FT CHAIN 22 >130 T-CELL RECEPTOR BETA CHAIN V REGION				
FT		A20.2.25.				
FT		FT DOMAIN 22 V SEGMENT.				
FT		FT DOMAIN 113 D SEGMENT.				
FT		FT DOMAIN 116 J SEGMENT.				
FT		FT CARBOHYD 36 POTENTIAL.				
FT		FT CARBOHYD 75 POTENTIAL.				
FT		FT NON_TER 130 SIGNAL 22 BY SIMILARITY.				
FT		FT SEQUENCE 130 AA; 14732 MW; 6721EC70DC64BEDB CRC64;				
FT						
FT		Query Match 9.7%; Score 161.5; DB 1; Length 130;				
FT		Best Local Similarity 30.4%; Pred. No. 5.3e-07;				
FT		Matches 41; Conservative 23; Mismatches 66; Indels 5; Gaps 3;				
FT						
FT		SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C;					
RC	MEDLINE; 84142271.	Qy 1 MGTRLLCWAALCLIGADHTGAGVSQTPSNKVTEKGKDVELRCDPISGHTALYWYROSGLQ 60				
RA	Hedrick S.M., Nielsen E.A., Kavalier J., Cohen D.I., Davis M.M.;	Db 1 MSCRLILYSLCLVETALMNTKTTQSPrVLGRA-NKSLECEQHLGHAMMYWQSAEK 59				
RT	"Sequence relationships between putative T-cell receptor polypeptides	Qy 61 GPEFLIYFGQGIAADDGLPNDRFAVPRPGSVSTLKRTEQDSDAANLRAVAGNWS 120				
RT	and immunoglobulins."	Db 60 PPELMFLYNLKOLIRNETVPS-RFIEPECDSKULLHISAVDPEDSAVYFCASSHG 115				
RT	Nature 308:153-158(1984).	RESULT 15				
DR	PIR; A02004; RWMS8.	ID I141_HUMAN				
FT	PFAM; PF00047; ig_1.	ID I141_HUMAN STANDARD; PRT: 213 AA.				
KW	T-cell; Receptor; Glycoprotein; Signal.					
FT	SIGNAL 1 21					
FT	CHAIN 22 133 T-CELL RECEPTOR BETA CHAIN V REGION 86T1.					
FT	DOMAIN 22 113 V SEGMENT.					
FT	DOMAIN 114 133 J SEGMENT.					
FT	CARBOHYD 36 36					
FT	CARBOHYD 75 75					
FT	DISULFID 41 109	BY SIMILARITY.				
FT	NON_TER 133 109					

AC P15814;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DE 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR.  
 GN IGL1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 [1]  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 89315835.  
 RA Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,  
 RA McLean J.P.;  
 RT "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are  
 expressed in pre-B cells and may encode the human immunoglobulin  
 omega light-chain protein";  
 RT Proc. Natl. Acad. Sci. U.S.A. 86:5552-5556(1989).  
 [2]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LYMPHOID;  
 RX MEDLINE: 91108327.  
 RA Evans R.J., Hollis G.F.;  
 RT "Genomic structure of the human Ig lambda 1 gene suggests that it may  
 be expressed as an Ig lambda 14.1-like protein or as a canonical B  
 cell Ig lambda light chain: implications for Ig lambda gene  
 evolution.";  
 RT J. Exp. Med. 173:305-311(1991).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN PRE-B-CELLS AND A SPECIAL  
 CC B-CELL LINE (WHICH IS SURFACE IG NEGATIVE).  
 CC -!- MISCELLANEOUS: THIS LAMBDA LIGHT-CHAIN-RELATED PROTEIN MAY BE THE  
 CC IMMUNOGLOBULIN OMEGA LIGHT-CHAIN.  
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SHOWS  
 CC SIMILARITY TO LAMBDA LIGHT CHAIN IN C-TERMINAL HALF (J AND C  
 CC REGIONS).  
 CC -----  
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 CC -----  
 DR EMBL; M27749; AAA61600; 1;  
 DR EMBL; M34513; ARA6096; 1;  
 DR EMBL; M34511; AAA6096; 1; JOINED.  
 DR EMBL; M34512; AAA6096; 1; JOINED.  
 DR PIR; A33911; A33911.  
 DR HSSP; P01842; 7FAB.  
 DR PFAM; PF00047; ig; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Immunoglobulin domain; B-cell; Signal.  
 FT SIGNAL 1 ?  
 FT CHAIN 213 IMMUNOGLOBULIN-RELATED 14.1 PROTEIN.  
 FT DOMAIN 97 108 J REGION (BY SIMILARITY TO LAMBDA  
 FT DOMAIN 109 213 LIGHT-CHAIN.  
 FT DOMAIN 109 213 C REGION (BY SIMILARITY TO LAMBDA  
 FT DOMAIN 109 213 LIGHT-CHAIN).  
 SQ SEQUENCE 213 AA: 22963 MW: 9133A742B943C79 CRC64;

Query Match 9.6%; Score 160.5; DB 1; Length 213;  
 Best Local Similarity 36.6%; Pred. No. 1.2e-06;  
 Matches 41; Conservative 18; Mismatches 44; Indels 9; Gaps 5;  
 Matches 41; Conservative 18; Mismatches 44; Indels 9; Gaps 5;

QY 126 FGPGTRITYLEDIKNVFPPEVAVFEPSEAFSTOKATLYCLATGFPDHYELSWWNGK 185  
 Db 98 FGSGTQLIVLSPQHAT - P-SVTLEPPSSEEL-QANKATLCLMNDFPGLITVTKADGT 154

QY 186 EVHSGVSTDPOPIKQEPAINDSFYCLSSRLYSATFQNPNRHERQOQEVG 237  
 Db 155 PITQGVEM-TTPSKQ --- SNKYAASSYSLTPEQNR-RRSYSQCMHKG 200

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OM protein - Protein search, using sw model

Run on: October 11, 2000, 06:08:41 ; Search time 18.52 Seconds  
(without alignments)  
1583.125 Million cell updates/sec

Title: US-09-405-940-1  
Perfect score: 1664  
Sequence: 1 MGTRLICWAALCLLGADHTG . . . . . AYLVSAEVLMAAVKRKDSRG 314

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues  
Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_14;\*

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1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rabbit:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

```

Q9qy93 rattus norv

Q31257 rattus norv

Q31266 rattus norv

Q31258 rattus norv

Q19446 rattus norv

Q95459 rattus norv

Q61832 mus musculu

P79587 rattus norv

Q9up60 homo sapien

Q9q57 mus musculu

P97797 mus musculu

Q95557 peromyscus

Q64272 mus musculu

Q95565 rattus norv

Q9ry91 rattus norv

Q9yp8 rattus norv

Q31149 mus musculu

Q9qx57 mus musculu

Q31254 rattus norv

Q99603 homo sapien

Q99604 homo sapien

Q31188 mus musculu

Q61642 mus musculu

Q31593 salmo salar

Q46632 bos taurus

Q61896 mus musculu

Q31272 rattus norv

## ALIGNMENTS

RESULT	1
Q9RIAS	PRELIMINARY;
ID ORIAs	PRT;
AC	214 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)	
DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update)	
DT 01-MAY-2000 (TREMBLrel. 14, Last annotation update)	
DE KAPPA LIGHT-CHAIN OF MAB7 (FRAGMENT).	
OS Mus musculus (Mouse)	
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus [1]	
RN SEQUENCE FROM N.A.	
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scrv).	
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.	
RL DR EMBL; AF15371; AAD40424.1; -.	
DR INTERPRO; IPR000495; -.	
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.	
FT NON_TER 1	214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
FT NON_TER 1	214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
DR INTERPRO; IPR00006; -.	
DR PROSITE; PS00047; iq; 2.	
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.	
FT NON_TER 1	214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
FT NON_TER 1	214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
DR INTERPRO; IPR000495; -.	
DR PROSITE; PS00047; iq; 2.	
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	181	10.9	214	11 Q9RIAS	Q9rla5 mus musculu
2	177.5	10.7	259	13 Q9RIAS	Q90530 ginglymosto
3	166	10.0	268	13 Q90524	Q90524 ginglymosto
4	165.5	9.9	267	13 Q90529	Q90529 ginglymosto
5	161	9.7	257	13 Q90536	Q90536 ginglymosto
6	156.5	9.4	437	11 Q9RIAA	Q9rla4 mus musculu
7	155.5	9.3	252	13 Q90568	Q90568 ginglymosto
8	154	9.3	684	13 Q90544	Q90544 ginglymosto
9	146.5	8.8	509	11 Q98907	Q98907 mus musculu
10	145.5	8.7	137	4 Q9UDR1	Qudr1 homo sapien
11	145.5	8.7	333	7 Q31522	Q1522 poecilia re
12	145.5	8.7	509	11 Q9WTN4	Q9wtm4 mus musculu
13	145	8.7	345	7 P79599	P79599 rattus norv
14	142.5	8.6	361	7 Q62896	Q62896 ictalus p
15	142	8.5	348	7 Q46835	Q46835 rattus norv
16	141.5	8.5	237	3 Q90545	Q90545 ginglymosto
17	141.5	8.5	346	7 P78088	P78088 rattus norv
18	141.5	8.5	367	7 P79589	P79589 rattus norv
19	141	8.5	296	7 Q31274	Q31274 rattus norv

Db	96	FTFGSGTKL---EIKRADAAPTVSIFPPSSSEOLT-SGGASVVCFLNNFYPDINYWKWI	150	CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Qy	183	NGKEVHSGV-STDPQPLKEQPALNDSRCLSSRLRVATWFQNPRNHERCQ	232	OC	Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
Db	151	DGSERQNGYLNSTMWDQDSK ---DSTYSSMSTLTIRDETER-HNSYTC	195	OC	Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
RESULT	2			RN	[1] SEQUENCE OF 1-240 FROM N.A.
ID	Q90530	PRELIMINARY;	PRT;	RP	SEQUENCE OF 1-240 FROM N.A.
AC	Q90530;			RC	TISSUE=SPLEEN;
DT	01-NOV-1996	(TREMBLrel. 01, Created)		RT	"A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks";
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		RL	Nature 374:168-173(1995).
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)		RN	[2] SEQUENCE FROM N.A.
DE	NOVEL ANTIGEN RECEPTOR (FRAGMENT).			RP	TISSUE=SPLEEN;
OS	Ginglymostoma cirratum (Nurse shark);			RC	Greenberg A.S.;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;			RA	Flajnik M.F.;
OC	Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;			RA	Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
OC	Orectolobiformes; Ginglymostomatidae; Ginglymostoma.			RL	EMBL; U18680; ARB48552.1; -.
RN	[1]			DR	HSSP; P01842; 7FAB.
RP	SEQUENCE OF 1-235 FROM N.A.			DR	INTERPRO; IPR00495; -.
RC	TISSUE=SPLEEN;			DR	INTERPRO; IPR003006; -.
RX	95183140.			DR	PFAM; PF00047; 19; 2.
RA	Greenberg A.S., Avila D., Hughes M., McKinney E.C.,			DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
RA	Plajnik M.F.;			ET	NON_TER 268 / 268
RT	"A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";			Score	10.0%
RT	extensive somatic diversification in sharks.";			Best Local Similarity	26.1%
RL	Nature 374:168-173(1995).			Matches	74; Conservative 38; Mismatches 121; Indels 50; Gaps 13;
RN	[2]			Qy	21 AGVSQTPSNKVTEKGDKDVEILRCDPESGRHAL--WYVYRSLSGQPEFLYFQGTGAADD
RP	SEQUENCE FROM N.A.			Db	77 19 ARVDQTPOEITKETGEISLISINCVLRDSNCALPSYWNRKSGSTNEETLSKG ---71
RC	TISSUE=SPLEEN;			Qy	78 GLPNDRFFAVRPEGESVST-TKIKQTEQQGSAAYIRAGVAGWSYYN--EQ----VFGP 128
RA	Greenberg A.S.,			Db	72 ----RYVETVYNSGSKSFSLRINDLTVESGTYROCKVKNW AYDCGLEELDMIYVYG 125
RA	Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.			Qy	129 GTRTLVLEDLKNVFPPEVAVFEPSEAEIISHTOKATLVCLATGFPDHYLSWNVNGKRVH 188
RL	EMBL; U16867; AAB48358.1; -.			Db	126 GTGVIVNPGLP-LSPPIVSLHSATEEQRANGFOLVCLLISGYPENAVSWRNTKT 184
DR	HSSP; P01842; 7FAB.			Qy	189 SGVSTDPOPLKEQPALNDSRCLSSRLRVATWFQNPRNHERCQYFGILSEND---EW 244
DR	INTERPRO; IPR003006; -.			Db	185 SGFAT-TSPYK--TSND - FSCASLLKPQLENSR-GSVYSSVHSATSSNRQEIR 238
DR	PFAM; PF00047; 19; 2.			Qy	245 TODRAKPTIQVSARWGRADCGFTSESYQGVHSATILYEIL 287
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			Db	239 TSEIAVLLRDFVTIWIWK-----SATLYCEVL 267
FT	NON_TER 259			RESULT	4
SEQUENCE	259 AA; 28245 MW;	07FF9860A92318B6E CRC64;		ID	Q90529 PRELIMINARY; PRT; 267 AA.
Qy	76 DSGLPDNDRFAVREPGESVSYTLKQRTEGDSAYLRAQVAAGWSYYNEQYF ---GPGT 130			AC	Q90529 PRELIMINARY; PRT; 267 AA.
Db	65 ENI1GGGRY--VETVNSQNLINDTIVEDGTYRCGGSLYNWCSTDVFLYARGAGT 122			DT	01-NOV-1996 (TREMBLrel. 01, Created)
Qy	131 RLTLEDLKNVFPPEVAVFEPSEAEIISHTOKATLVCLATGFPDHYLSWNVNGKRVH 190			DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
Db	123 AVIVNPGIP-PSPIPVSLHSATEQRANRFTVQLVCLISGYPENAVSWRNTKTSG 181			DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
Qy	191 VSTDPQPLKEQPALNDSRCLSSRLRVATWFQNPRNHERCQYFGILSEN 241			DE	NOVEL ANTIGEN RECEPTOR (FRAGMENT)
Db	182 FAT-TSPVK--TSND - FSCASLLKPQLENSR-GSVYSSVHSATSSN 226			OS	Ginglymostoma cirratum (Nurse shark).
RESULT	3			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
ID	Q90524	PRELIMINARY;	PRT;	OC	Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
AC	Q90524;			OC	Orectolobiformes; Ginglymostomatidae; Ginglymostoma.
DT	01-NOV-1996	(TREMBLrel. 01, Created)		RN	[1] SEQUENCE OF 1-243 FROM N.A.
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		RC	TISSUE=SPLEEN;
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)		RA	Greenberg A.S., Avila D., Hughes M., McKinney E.C.,
DE	NOVEL ANTIGEN RECEPTOR (FRAGMENT).			RA	Plajnik M.F.;
OS	Ginglymostoma cirratum (Nurse shark)			RT	"A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in shark.";
				RL	Nature 374:168-173(1995).

Q90568	Best Local Similarity 27.0%; Pred. No. 2.7e-07; Matches 63; Conservative 31; Mismatches 105; Indels 34; Gaps 10;
RC	SEQUENCE FROM N.A.
TISSUE=SPLEEN;	
Greenberg A.S.;	
Submitted (DEC-1994) to the EMBL/GenBank/DBDJ databases.	
EMBL: U18693; AAB48367.1; - .	
HSSP: P01842; 7FAB;	
INTERPRO: IPR000495; - .	
INTERPRO: IPR003006; - .	
PFAM: PF00047; iq; 2.	
PROSITE; PS00290; IG_MHC; UNKNOWN_1.	
NON_TER 267 267	
SEQUENCE 267 AA; 29402 MW; OE1362456E22CB94 CRC64;	
Q90568	Query Match Score 9.9%; Score 165 5; DB 13; Length 267; Best Local Similarity 26.9%; pred. No. 1.1e-07; Matches 63; Conservative 36; Mismatches 100; Indels 35; Gaps 11;
23 VSQTPSNKVKTEKGKVDELRC --DPDLSGHFTALWYRQSLGQPEFLIFQGTGAAADDGL 79	RESULT 6
21 VDQTPHSITKTGEHTSTINCVLRSACGLSNAQNYRERSGSTKEENI -SGCARYVE---- 75	Q9R1A4 PRELIMINARY; ID Q9R1A4; AC Q9R1A4; PRRT; 437 AA.
DDB YY 80 PNDRFTAVRPQGSVSTKLKIQRTEQGDSAAVLRAGYAAGW-----SSNEYQ -FG 127	DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
DDB YY 76 -----TVNRESKSFLRINDLTVEDSGS` -RCMASTWTDIEGGLELGPCTNCQHDVYQ 127	DT 01-JUN-2000 (TREMBLrel. 14; Last annotation update)
DDB YY 128 PGTRIVDLEDKNVPPEVAFPEPSEAEIHTQTAKLVCLATGFDPDHVELSWAVNGKEYV 187	DR GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
DDB YY 128 ADTVVTPVNGGP-LSPPIVSLLHSATEQRANGFQVLCLISGYPPENTAVSQNKNTKI 186	OS Mus musculus (Mouse).
DDB YY 188 HSGVSTDPOPLKEQPALNDSRYCLSSRLRVSATFWQNPRNHRFCQVQFYGLSEN 241	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]
DDB YY 187 TSGFAT-TSPVK--TSSND-- -FSCASLLKVPLOEWSR-GSYSCOVSHSATSSN 234	RN SEQUENCE FROM N.A.
DDB YY 29290536 PRELIMINARY; PRT; 257 AA.	RP Ekramoddoullah A.K.M.; Misra S.; Wilde K.G.; Yu X.; DR Submitted (MAY-1999) to the EMBL/GenBank/DBDJ databases. EMBL: AF15372; AAD04243.1; -.
DDB YY 29290536 Q90536 PRELIMINARY; PRT; 257 AA.	DR INTERPRO; IPR000495; - .
DDB YY 29290536 Q90536 AC 01-NOV-1996 (TREMBLrel. 01, Created) 01-NOV-1996 (TREMBLrel. 01, Last sequence update) 01-JUN-2000 (TREMBLrel. 14, Last annotation update)	DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DDB YY 29290536 DE NOVEL ANTOGEN RECEPTOR (FRAGMENT).	FT NON_TER 1 1
DDB YY 29290536 DS Ginglymostoma cirratum (Nurse shark).	FT NON_TER 437 437 AA; 48142 MW; SQ SEQUENCE 437 AA; 48142 MW;
DDB YY 29290536 DC Eulambranchii; Metazoa; Chordata; Vertebrates; Chondrichthyes; Orectolobiformes; Ginglymostomatidae; Galeoidea; Orectolobiformes; Ginglymostomatidae; Ginglymostoma. [1]	Query Match Score 9.4%; Score 156 5; DB 11; Length 437; Best Local Similarity 27.1%; pred. No. 1.5e-06; Matches 58; Conservative 33; Mismatches 98; Indels 25; Gaps 10;
DDB YY 29290536 RN SEQUENCE OF 1-242 FROM N.A.	Q90568
DDB YY 29290536 TISSUE=SPLDEN;	Q90568 Best Local Similarity 27.0%; Pred. No. 2.7e-07; Matches 63; Conservative 31; Mismatches 105; Indels 34; Gaps 10;
DDB YY 29290536 RX MEDLINE; 95183140.	Q90568 QTPSNKVKTEKGKVDELRC --DPDLSGHFTALWYRQSLGQPEFLIFQGTGAAADDGL 80
DDB YY 29290536 RA Greenberg A.S.; Avila D.; Hughes M.; McKinney E.C., Flajnik M.F.; "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.", Nature 374:168-173 (1995).	Db 4 QESGGGIVKPGGSLISC-AASGEFESSYMSWWQTPPERLKENVAFESSGGGIIYYTDSY 62
DDB YY 29290536 RN SEQUENCE FROM N.A.	Q90568 NDREFFAVR -PEGSVSTKLKIQRTEQGDSAAVLRAGYAAGWSSYNEQFGPSTRVLYIEDLK 139
DDB YY 29290536 RC Submitted (DEC-1994) to the EMBL/GenBank/DBDJ databases.	Db 63 KGRFTYKDRNLSLQMSSRLSDTAMYCAR---GDYS AWGPOPLTVTY-SAA 114
DDB YY 29290536 RL HSSP; P01842; 7FAB;	Q90568 140 NVEPPFVAVFPSEAEIHTQTAKLVCLATGFDPDHVELSWAVNGKEYVHSGVSTDPQPK 199
DDB YY 29290536 DR INTERPRO; IPR000495; - .	Db 115 KTPPPSVYPAPGSAQTNM-vtGCLVYGYFPBVTVW- -NSGSLSSGVHTRP--- 167
DDB YY 29290536 PRFAM; PF00047; iq; 2.	Q90568 200 EQPALNDSRYCLSSRLRVSATFWQNPRNHRFCQV 233
DDB YY 29290536 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.	Db 168 -AVQSDLTLSSVTPTSTW- -PSETVTCNV 197
DDB YY 29290536 FT SEQUENCE 257 AA; 28083 MW; BAO019A99D0BC491 CRC64; RESULT 7	Q90568 ID Q90568 PRELIMINARY; PRT; 252 AA.
DDB YY 29290536 FT SEQUENCE 257 AA; 28083 MW; BAO019A99D0BC491 CRC64; Query Match 9.7%; Score 161; DB 13; Length 257;	

DT	01-NOV-1996 (TREMBLrel. 01, Created)	RL	Nature 374:168-173(1995); DR EMBL; U18701; AAB4195..1; -.
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)	DR	INTERPRO; IPR003006; -.
DS	NOVEL ANTIGEN RECEPTOR (FRAGMENT)	DR	INTERPRO; IPR0047; 19; 6;
OC	Ginglymostoma cirratum (Nurse shark)	DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes	KW	SIGNAL.
OC	Orectolobiformes; Neoselachii; Galeoidea; Ginglymostoma	FT	1 18 POTENTIAL.
RN	[1]	FT	19 NOVEL ANTIGEN RECEPTOR.
RC	SEQUENCE OF 1-239 FROM N.A.	SQ	SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDAD6DFD CRC64;
RX	TISSUE=SPLEEN; MEDLINE; 95183140.		
RA	Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.; "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";	Query Match 9.3%	Score 154; DB 13; Length 684; Best Local Similarity 22.8%; Pred. No. 4.7e-06; Matches 64; Conservative 41; Mismatches 110; Indels 66; Gaps 12;
RL	Nature 374:168-173(1995), [2]	Qy	23 VSQTPSNKVKTEKGDKDVELRC-----DPISGHTALWYROSLSQGPEFLIFQGTGAAD 75
RN	SEQUENCE FROM N.A.	Db	21 VDQTTPSVAKEAGQVITNCVLRGANYEAKGSTC---WPKKSG-----SKVE 66
RC	TISSUE=SPLEEN;	Qy	76 DSGLPNDRFFAVRPESVS-TLKIQRTEQGDSAAYLragvaAGGSNSYNDQYF---- 126
RA	Greenberg A.S.;	Db	67 ESITKGGRYYETVNNSKSFSLRINDLTEDAGDYL---CAAMEAADCMYGYCTIYPF 122
RL	"A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";	Qy	127 ---GIGTRLVLEDILKVNPEPEVFPSEATSHQATLYCLATGYPDHVLSWIV 182
RL	Nature 374:168-173(1995), [2]	Db	123 SGACGSGTAGTVTPGP-PSPPIVSLLHSATEQRANRFVQLCLISGYPENTAVSNK 181
RN	SEQUENCE FROM N.A.	Qy	183 NCKEVHSGVSIDPQPLKEQPALNDSDRYCLSSRLRSATFWQNPNRHFCRQVQYGLSEN 242
RC	Flajnik M.F.;	Db	182 NTKTITSGPAT-TSPVKT-TSSND-FSCASLKVPLQWSR-GSVIQQVSHSATSSN 235
RA	"A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";	Query Match 9.3%	Score 155.5; DB 13; Length 252; Best Local Similarity 27.6%; Pred. No. 8.6e-07; Matches 64; Conservative 31; Mismatches 102; Indels 35; Gaps 11; Gaps 11;
DR	HSSP; P01842; 7FAFB	RESULT 9	WTQDRAKPTQIVSAEWG 262
DR	INTERPRO; IPR00495; -.	ID	008907 PRELIMINARY; PRT; 509 AA.
DR	INTERPRO; IPR003006; -.	AC	008907; PRELIMINARY; PRT; 509 AA.
DR	PFAM; PF00047; ig; 2.	DT	01-JUL-1997 (TREMBLrel. 04, Created); DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DR	PSO0192; IG_MHC; UNKNOWN_1.	DE	DE BRAIN IMMUNOLOGICAL-LIKE PROTEIN (BIT).
DN	TER; 252	GN	GN BIT.
TER	252 AA: 27356 MW; 117F2225B2E17EDF CRC64;	OS	OS Mus musculus (Mouse).
SEQUENCE	252 AA: 27356 MW; 117F2225B2E17EDF CRC64;	OC	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RC		RN	RN [1]
RA		RP	SEQUENCE FROM N.A.
RA		RC	STRAIN-BALB/C; TISSUE=BRAIN;
RA		RX	MEDLINE: 97230468.
RA		RT	"BIT (Bit) maps to mouse chromosome 2.";
RL	Genomics 40:504-506(1997).	RL	Genomics 40:504-506(1997).
DR	D85785; BAA20376..1; -.	DR	D85785; BAA20376..1; -.
DR	MGD; MG1:107947; Bit.	DR	MGD; MG1:107947; Bit.
DR	INTERPRO; IPR00495; -.	DR	INTERPRO; IPR00495; -.
DR	INTERPRO; IPR003006; -.	DR	INTERPRO; IPR003006; -.
DR	PFAM; PF00047; ig; 3.	DR	PFAM; PF00047; ig; 3.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.	DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ	SEQUENCE 509 AA; 56033 MW; 1E377ACBEC31BA13E CRC64;	DB	SEQUENCE 509 AA; 56033 MW; 1E377ACBEC31BA13E CRC64;
RN	SEQUENCE FROM N.A.	Query Match 8.8%	Score 146.5; DB 11; Length 509; Best Local Similarity 22.4%; Pred. No. 1.6e-05; Matches 95; Conservative 58; Mismatches 132; Indels 139; Gaps 24;
RC	SEQUENCE-SPLEEN;	Qy	1 MGTRLLC-WAALCL-LGADHTGAGVQSPPSNKYTEKGDKVELRCD---PISGHNTALY 52
RC	MEDLINE; 95183140.	Db	11 LGPLLCILLSSACRGTGATGTEKVTPQEKSVAAAGGSTLNLCTVTSLLPVG---PIR 67
RA	Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.; "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";		

QY	53	WYROSIGQGEEFLIFYFQGSGA-----ADDSGLPNDRFAVR-----PE- GSYSTIKI	98	66 -TYFGQTGAADDSSGLPNDRFAVR- PEGSVSTLKIQRTQGDSSAYALRAGVAAGWSYY 122
Db	68	WYR-- -GVGQSLRLSYYSETEHEPRVRNSDTSKRNMDSEFIRISNTVYDAGIYTCVKF 124	Db	70 VSISYDG-T-VRKESSIPSGKFEVDRIPESTSTLTINVEKQDIATY---YCALWEVHS 124
QY	99	QR-TEQGDSAYLRAVGANGWSSYNEQYFPGPTRLTVLEDLKNFVEPPVAFERSEAETS 157	QY	123 EQYFGPGRTRLY 134
Db	125	QRGSSEPTD-----EIQSGGGTENVY--LAKTSPPEYS- -GADRGP 163	Db	125 SRQFBPSHSINV 136
QY	158	HTQRKATLVCLATGFYPDHVLSWVNGKEYH-----SG-----VSTDQPLKEQFA 203	RESULT 11	
Db	164	-DQKVNFTCKSHGFSPRNITLKWFDQGEHPLETTVNPSGKAVSYNISSTVRYVLNSHD 222	Q31522	PRELIMINARY; PRT; 333 AA.
QY	204	LNDSYRC-----LSSRURVSAT-FWNP-----RNHFRCQ----- 232	ID Q31522	
Db	223	VNSKVTCVEAHITLDSPLEGIANSNFIRSPVTKVTPPPTSMQNQVNITCRARFYTYPE 282	AC AC1522;	
QY	233	-VQFYGGLSENDEWTODRAKFTVQ-----IVSAFAWGRADCGET----- 269	DT DT01-NOV-1996 (TREMBLrel. 01, Created)	
Db	283	DQLIWLENNSVNSRSDTPKALTKNIDGTNYTTSFLVNSA -HREDVVETCQVKHDDQQA 341	DT DT01-MAY-1996 (TREMBLrel. 01, Last sequence update)	
QY	270	-----SESYQGVL-----SATILEYLIG--KATLVAVLSVALVNAMEVKK 310	DT DT01-MAY-2000 (TREMBLrel. 13, Last annotation update)	
Db	342	ITRNHTVGLAHSSDQGSMOTFPGNATHNWNVF1GTVGYACALLVILMAALYLIRQK 401	DE MHC CLASS IA (FRAGMENT).	
Qy	311	DSRG 314	OS Poecilia reticulata (Guppy).	
Db	402	KAKG 405	OC Eukaryota; Metzcoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleosteoi; Euteleostei; Acanthopterygii; Otherincormpha; Cyprinodontiformes; Cyprinodontidae; Poeciliidae; Poecilia.	
RN			RN [1]	
RX			SEQUENCE FROM N.A.	
RA			RX MEDLINE: 96128251.	
SA			RA Sto A.; Figueroa F.; O'Huigin C., Reznick D.N., Klein J.;	
RT		"Identification of major histocompatibility complex genes in the	RT RT	
RL		Poecilia reticulata."	RL ImmunoGenetics 43:38-49 (1996).	
EMBL			DR IMBL; 254085; CAA0791_1; -.	
INTERPRO			DR IPIR001039; -.	
IPR003006			DR IPR003006; -.	
PFAM			DR PFAM; PF00047; 19; 1.	
MHC			DR PFAM; PF00129; MHC_I; 1.	
FT			KW MHC.	
SEQUENCE			FT NON_TER	
			SQ SEQUENCE 333 AA; 37165 MW; D9C942B504B8014D CRC64;	
Query Match			Query Match Similarity 8.7%; Score 145.5; DB 7; Length 333;	
Best Local Similarity			Best Local Similarity 22.1%; Pred. No. 1,1e-05;	
Matches			Matches 34; Mismatches 34; Indels 107; Gaps	
Q9UDR1			Q9UDR1	
AC			AC YRQSLGQGPPEFLIYFQGTGAADDSSGLPNDRFAVRPEGSYSTLKIQRTQGDSSAYLRA 113	
OSUDR1			OSUDR1	
DT	01-MAY-2000 (TREMBLrel. 13, Created)		DT 113 YTFQFGMDGDDESVF-----DLKTESWTAPEAVVTTWHDNDK-----G 152	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		DT 153 LNAGMVNYLTQNCPPEWKKVVNYGR-----SSLMRTVPPSVL-----LQMSSSPVS 200	
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		DT 166 CLATGFPDHVELSKWVNGKEVHSGYSTDPQPLKEQPALNDSYCLSSLRVRSTATWQNP 225	
DE	T-CELL RECEPTOR GAMMA CHAIN, TRGVY,		DE 201 CYATSFYPNRFEMILWRKG-----ELIPRNDDTQMSVLTISK----- 249	
OS	Homo sapiens (Human).		OS 226 RNFHQCVQFYGLSENEDTQDRAPVTQIVSAEWGRADCGFTSESYQGVQLSATILYE 285	
OC	Eukaryota; Metzcoa; Chordata; Craniata; Vertebrata; Euteleostomi;		OC 250 -----S-----SEDWTKDCVFLQLSGVDFKDVL----- 270	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		OC 286 ILLGKA-----TLYAVV-----SALVLMAMYKRKDSR 313	
RN			RN 271 IPDRANIKTNAGNSLALITIVAVVLTISAVIVLVRKKAK 315	
RP			RP RESULT 12	
RP			RP C9WTNA PRELIMINARY; PRT; 509 AA.	
RA			RA ID Q9WTNA	
RA			RA AC Q9WTNA;	
RT	"Toward a complete human genome sequence.";		RT DT 01-NOV-1999 (TREMBLrel. 12, Created)	
RL			RL DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)	
RN			RN DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)	
RP			RP DE BIT.	
SEQUENCE FROM N.A.			SEQUENCE FROM N.A.	
Arnett C., Wohldmann P., Le T.; "The sequence of Homo sapiens BAC clone RP11-121A8.";			Arnett C., Wohldmann P., Le T.; "The sequence of Homo sapiens BAC clone RP11-121A8.";	
RT			RT RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RT			RT RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RL			RL RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RN			RN RN Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RP			RP RP Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RL			RL RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RN			RN RN Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RP			RP RP Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RA			RA RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RA			RA RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RT			RT RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RT			RT RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
RL			RL RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	
AC006033; AAC05557; 1.			AC006033; AAC05557; 1.	
INTERPRO	IPR003006;		INTERPRO IPR003006;	
PFAM	PF00047; ig; 1.		PFAM PF00047; ig; 1.	
Receptor.			Receptor.	
SEQUENCE	137 AA; 15184 MW; B1FF9F63D3671609 CRC64;		SEQUENCE 137 AA; 15184 MW; B1FF9F63D3671609 CRC64;	
Query Match			Query Match Similarity 8.7%; Score 145.5; DB 4; Length 137;	
Best Local Similarity			Best Local Similarity 33.3%; Pred. No. 3,2e-06;	
Matches	44;	Conservative 19; Mismatches 52; Indels 17; Gaps	Matches 44; Conservative 19; Mismatches 52; Indels 17; Gaps	7;
Q10	ALCLGDAHDHGAGYQTSPTSNKVTERGKDYELRCDFISG-----HTALWYRQSQGQPEFL 65		Q10 ALCLGDAHDHGAGYQTSPTSNKVTERGKDYELRCDFISG-----HTALWYRQSQGQPEFL 65	
Db	15 ALCYVAGH----LQPQISTKTLSKTARLEC-VVSGTISATSVYWRERPGVQVNL 69		Db 15 ALCYVAGH----LQPQISTKTLSKTARLEC-VVSGTISATSVYWRERPGVQVNL 69	

BIT. Mus musculus (Mouse). OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1] RSP STRAIN=C57BL/6; TISSUE=BRAIN; RA Sano S.; RT "Mouse type III BIT."; RL Submitted (Oct-1998) to the EMBL/GenBank/DDBJ databases. EMBL: AB018184; NRA76555.1. DR INTERPRO; IPRO00095; -. DR INTERPRO; IPRO003006; -. DR PEAM; PF00047; ig\_1. DR PROSITE; PS00290; IG\_RHC; UNKNOWN\_1. SQ SEQUENCE 509 AA; 55986 MW; CFSASEC9404C14CF CRC64;

Query Match 8.7%; Score 145; DB 7; Length 345; Best Local Similarity 22.8%; Pred. No. 1..3e-05; Matches 56; Mismatches 104; Indels 84; Gaps 16; Matches 72; Conservative 56; MisMatches 16; Gaps 16;

Query 1 MGRFLIC -WAALCL-LGADHTGAGYSQTOPSNKVTEKGKDVLRCR----PISGHTALY 52 DR 11 LGPLLCULLSSCPCTGATGKBLKTQPEKSVYAAGDSTVNLCLTSLIPVG --PIR 67

Query 53 WYROSIGQGPFLIYFQGTGA-----ADDGSLPNDRFFAVRPEGSVSTLKIQTREQGD 105 DR 68 WYR---GVGPRSLIYSSAGEYVPRTRNSDITKRNMDFSR-----ISNVTPAD 115

Query 106 SAAYLRAVGAAGWSYYN-EQYQGPGLTLELDLKVNFPPEVAVEPSEAFISHPOKATL 164 DR 116 AGIYYCYKFQKGSSEPEDEIQGGTTEVYV--LAKPSPPVS--GPADRGIP-PQKVNF 169

Query 165 VCATGFPDHLVEWLSWAWNGKEHV-----SG-----VSDPDLPOPILKEPALNDNSRC 210 DR 170 TCKSHGFSPRNTLKWWDQGELHPLLETTVAFSGKNVSYNTSTRVVLNSMDVNSKVIC 229

Query 211 -----LSSRLRVSATE--WQNPRN----HERCQ-----VQFYGL 238 DR 230 EVAHITLDRSPRLGIANLNSNFTRVSPIVKVTQCSPTSMQVNLTCHAERFYPEDLQLIWL 289

Query 239 SENDEWQDRAPVTO-----IVRAEANWRADCOT----- 269 DR 290 ENGNVSRNDTPPNLTKNDGTWNTSLFLYNSA HREDVVFTCOVKHDQOPATRNRHTV 348

Query 270 --SESYOQGV-----SATIYLELLG--KATLYAVLYSALVLMAMYKRKDSRG 314 DR 349 LGAHSSDQGSMOTFPDNNATHNWYFIGVACALLVLLIMAAYLLRKKKAKG 405

RESULT 13 DR P79599 PRELIMINARY; PRT; 345 AA. RN P79599 ID PRELIMINARY; PRT; 345 AA.

AC Q9554; DT 01-MAY-1997 (TREMBrel. 03, Created)

DT 01-MAY-1997 (TREMBrel. 03, Last sequence update)

DT 01-MAY-2000 (TREMBrel. 13, Last annotation update)

DE MAURO ALPHA CHAIN OF MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I

GN R71A1. OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. [1]

RN SEQUENCE FROM N.A.

RP SPAIN=PT1(0); ISSUE=SPLEEN; RA Joly E., Le Rolle A.F., Gonzalez A.L., Mehling B., Stevens J., Corwell W.J., Huenigen T., Howard J.C., Butcher G.W.; Curr. Biol. 0:0-0(1999). EMBL: X90373; CA662023.1; HSSP; P01900; IBILI; INTERPRO; IPRO00095; -. DR

DR INTERPRO; IPRO01039; -. DR INTERPRO; IPRO03006; -. DR PEAM; PF00047; ig\_1. DR PROSITE; PS00290; IG\_RHC; UNKNOWN\_1. KW MHC. FT NON\_TER SQ SEQUENCE 345 AA; 39221 MW; 9A28E9E36993A7C8 CRC64;

Query Match 8.7%; Score 145; DB 7; Length 345; Best Local Similarity 22.8%; Pred. No. 1..3e-05; Matches 56; Mismatches 104; Indels 84; Gaps 16; Matches 72; Conservative 56; MisMatches 16; Gaps 16;

Query 25 QTPSNKVTBKGKDVLRLRTRGYNQSEGSHSTIOEMYGDVGDSLLRQGYRDAYGDR 122 DR 63 ETQNAKENEVYRYRDLTRLGRGPE-VAVFEPSEAEISHTOKATLVCLATGFYDPDVEL 178

Query 64 FLIYFQG--TGAADDGSLPNDREFAVRPGSVSTLKIQTREQGDS-AAYLRAVGAWS S 120 DR 123 YIALNEDLKTWTAA----FAAQ----TRNKWEBAKYAERLRQLQ GTCVEML 168

Query 124 YNEQYFGPSTRLTYLEDLKNEVPE----CDPISGHTALYWYROSLLGCGPE 63 DR 169 --RRLYLEGKETLRSRSD----PKAHVTLHPREGDV----TLCWALGHYPADISL 215

Query 179 SWVNGKEYHSGYSTDPQPIKEQPALNDNSRCYCLSSRLRVATEFWQNPRNHFRCQFYGL 238 DR 216 SWQINGED----LQDMELIVETRPA-GDGTFRQWASVVVPLGREQN----YTCRVERHEGL 266

Query 239 SENDEWQDRAPVTOQIVSAEANGRADCGFTSESYQGVGLSALLYELLGRATLYAVL 298 DR 267 PE-----PLSQ-----RWEPLSTDSEN----METTVIYVVLGAVAIIAAVI 304

Query 299 SALVLMAMMYKRKDSRG 314 DR 305 GAVVAVVRRERRNTEG 320

RESULT 14 DR 062896 PRELIMINARY; PRT; 361 AA.

ID 062896 PRELIMINARY; PRT; 361 AA.

AC 062896; DT 01-AUG-1998 (TREMBrel. 07, Created)

DT 01-AUG-1998 (TREMBrel. 07, Last sequence update)

DT 01-JUN-2000 (TREMBrel. 14, Last annotation update)

DE MHC CLASS I ALPHA CHAIN

GN ICPU-E7.

OS Ictalurus punctatus (Channel catfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygi; Neopterigii; Teleosteoi; Buteleosteoi; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.

RN [1]

RP SEQUENCE FROM N.A.

RA Antao A.B., Chinchar V.G., McConnell T.J., Miller N.W., Clem L.W., Wilson M.R.;

RA Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

RL EMBL; AF03549; ADD08650.1; -. DR INTERPRO; IPRO01039; -. DR PEAM; PF00047; ig\_1. DR PRODOM; PD000050; -. DR MHC. KW MHC. FT NON\_TER SQ SEQUENCE 361 AA; 40914 MW; AB668B3F5A9CC1E6 CRC64;

Query Match 8.6%; Score 142.5; DB 7; Length 361; Best Local Similarity 25.1%; Pred. No. 2..4e-05; Matches 51; Conservative 32; MisMatches 73; Indels 47; Gaps 7;

Query 118 WSSNNE-----QYFGGTRLTVLEDIKNVFPPEAVFEPSEAEISHTOKATLVCLAT 169 DR

Db 178 WKNYLEKECIEWLOKRYVGYR-----ETLERKVPTASVQEES-----SPEVVCHAT 226  
 Qy 170 GFYDPDHVELWWNGKEVHSVGSTDPQPLIKEQPALNDSRYCLSSRLRVSYATEQNPNHF 229  
 Db 227 GFFPKTVMTIWWQKQEDHEDVE----LRETLPNQDGTEQKRSILYSAEIQ--KHTY 279  
 Qy 230 RCQVOFYGLESENDWTQDRAKPQTQIVSAEANGRADCGFTSESTQGYLSATILYEILG 289  
 Db 280 TCVIOHQSSL-----KENVLPSE-----RRILNPQGGSGVYLIGIV 318  
 Qy 290 KATLYAVLVSVLVALMAMYKRKDS 312  
 Db 319 VVAALLVLVAVVAGIVVWKKNS 341

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RESULT 15  
 046875 PRELIMINARY; PRT; 348 AA.  
 ID 046875 PRELIMINARY; PRT; 348 AA.  
 AC 046875;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DR 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE MHC CLASS IB ALPHA CHAIN PRECURSOR (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=PVG\_R19; TISSUE=SPLEEN;  
 RA Leong L.Y.W.; Deverson B.V.; Joly E.; Butcher G.W.;  
 RL Submitted (JUN 1997) to the EMBL/GenBank/DBJ databases.  
 DR HSSP1880; CAA74192.1; -.  
 DR HSSP1900; CAA74192.1; -.  
 DR INTEPRO; IPR00495; -.  
 DR INTEPRO; IPR001039; -.  
 DR INTEPRO; IPR001064; -.  
 DR INTEPRO; IPR003006; -.  
 DR PFAM; PF00047; ig; 1.  
 DR PFAM; PF00129; MHC\_I; 1.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Signal; MHC.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 3  
 FT CHAIN 4 348 AA; 39108 MW; MATURE MHC CLASS IB ALPHA CHAIN.  
 SQ SEQUENCE 348 AA; BDAC4D8880ED611E CRC64;

Query Match 8.5%; Score 142; DB 7; Length 348;  
 Best Local Similarity 25.3%; Pred. No. 2.5e-05;  
 Matches 7; Conservative 44; Mismatches 97; Indels 74; Gaps 15;  
 Matches 9; Conservation 75;

Qy 49 TALIWWRQSLQQGQPFLLYPOGTGAADDGL-----PNDRFAVRPEGSYSTLQR 100  
 Db 83 TLLRYNNQSEG-GSHTFQMSGODLSGDSLRLGYEQSAYNGDYIVNE-----DLKT 135  
 Qy 101 TEQGDSSAAY-----RAGYAGMISSNEYQQYFGPGTRIVL-----EDLRKNEFPE- 145  
 Db 136 WTAADTARPTTRNWKDRAGAERHKAYLE-----GTICLESYLELGKETLRSDPKA 190  
 Qy 146 -VAYFEPSEAEISHTQKATLVCATGIFYPDHVLSWVNGKEYHSGYSTDPOPPLKEOPAL 204  
 Db 191 HVTLHPRPQGDV----TLRCWALGFPGISLTWONGED---LJQDMELVETPA- 239  
 Qy 205 NDSRYCLSSRLRVSYATEQPRNHRFCQYOFYUSSENDWTQDRAKPQTQVSAEANGRA 264  
 Db 240 GDGPEQKWAQVVPPLGKEON----YTCLIVEBEGIPE-----PLTO-----RW 277  
 Qy 265 DCGFTSESESYQGVQVISATILEILLGKATLYAVLN SALVLMAMYKRKDSRG 314  
 Db 278 EPSPTDSN----METNVVYVILGAVATIGAVIAVTVVR KRRTNGG 322

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Gencore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.		Human TCRbeta prot. Sequence of T-cell Mouse A1 T cell re HLA-A2/flu restric TCR beta chain and Sequence encoded by HTLV-1 Tax/HLA-A2 HTLV tax/HLA-A2 re TCR beta chain and TCR beta chain and Mouse H2-DD/flu nu HLA-A2/flu gag res TCR beta chain and HTLV tax/HLA-A2 HTLV beta chain and HLA-A2/flu restric TCR beta chain and TCR beta chain and HLA-A2/flu restric TCR beta chain and TCR beta chain and HTLV-1 Tax/HLA-A2 HTLV tax/HLA-A2 re TCR beta chain and TCR beta chain and TCR beta chain and HTLV tax/HLA-A2 re TCR beta chain and Sequence of the be Mammalian T Lympho Cytotoxic T Lympho Murine cytotoxic T Single Chain T cell Human TCRbeta prot Murine TCRbeta pro Murine TCRbeta pro Murine TCRbeta pro					
OM protein - protein search, using Sw model	Run on: October 11, 2000, 06:08:06 ; Search time 15.62 Seconds (without alignments) 687.378 Million cell updates/sec	13	907	54.5	177	21	Y51068
Perfect score: 1664	Sequence: MGRLLCWAALCLLGADHTG.....AVLVSALVLMAMVKRKDSRG 314	14	896	53.8	306	6	P50252
Scoring table: BLOSUM62	Searched: 268485 seqs, 34193795 residues	15	883	53.1	314	20	Y05728
Minimum DB seq length: 0	Total number of hits satisfying chosen parameters: 268485	16	880	52.9	287	21	Y56077
Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0%	17	880	52.9	287	21	Y560753
	Maximum Match 100%	18	880	52.9	306	6	P50344
	Listing first 45 summaries	19	874.5	52.6	307	21	Y56059
Database : A_Geneseq_36.*		20	874.5	52.6	307	21	Y56083
1: /SIDSS6/gcqdata/geneseq/geneseq/AAI1980.DAT:*		21	874.5	52.6	307	21	Y57859
2: /SIDSS6/gcqdata/geneseq/geneseq/AAI1981.DAT:*		22	874.5	52.6	307	21	Y57868
3: /SIDSS6/gcqdata/geneseq/geneseq/AAI1982.DAT:*		23	873.5	52.5	287	21	Y56079
4: /SIDSS6/gcqdata/geneseq/geneseq/AAI1983.DAT:*		24	873.5	52.5	287	21	Y56081
5: /SIDSS6/gcqdata/geneseq/geneseq/AAI1984.DAT:*		25	873.5	52.5	287	21	Y57855
6: /SIDSS6/gcqdata/geneseq/geneseq/AAI1985.DAT:*		26	873.5	52.5	287	21	Y56057
7: /SIDSS6/gcqdata/geneseq/geneseq/AAI1986.DAT:*		27	870	52.3	287	21	Y56056
8: /SIDSS6/gcqdata/geneseq/geneseq/AAI1987.DAT:*		28	870	52.3	287	21	Y57865
9: /SIDSS6/gcqdata/geneseq/geneseq/AAI1988.DAT:*		29	870	52.3	305	21	Y56082
10: /SIDSS6/gcqdata/geneseq/geneseq/AAI1989.DAT:*		30	870	52.3	305	21	Y57866
11: /SIDSS6/gcqdata/geneseq/geneseq/AAI1990.DAT:*		31	870	52.3	306	21	Y56061
12: /SIDSS6/gcqdata/geneseq/geneseq/AAI1991.DAT:*		32	870	52.3	306	21	Y56085
13: /SIDSS6/gcqdata/geneseq/geneseq/AAI1992.DAT:*		33	870	52.3	306	21	Y57861
14: /SIDSS6/gcqdata/geneseq/geneseq/AAI1993.DAT:*		34	870	52.3	306	21	Y57870
15: /SIDSS6/gcqdata/geneseq/geneseq/AAI1994.DAT:*		35	869.5	52.3	307	21	Y56086
16: /SIDSS6/gcqdata/geneseq/geneseq/AAI1995.DAT:*		36	869.5	52.3	307	21	Y57862
17: /SIDSS6/gcqdata/geneseq/geneseq/AAI1996.DAT:*		37	868.5	52.2	293	7	P60238
18: /SIDSS6/gcqdata/geneseq/geneseq/AAI1997.DAT:*		38	868.5	52.2	293	10	P91815
19: /SIDSS6/gcqdata/geneseq/geneseq/AAI1998.DAT:*		39	868.5	52.2	293	18	W01532
20: /SIDSS6/gcqdata/geneseq/geneseq/AAI1999.DAT:*		40	868.5	52.2	293	21	Y50114
21: /SIDSS6/gcqdata/geneseq/geneseq/AAI2000.DAT:*		41	827	49.7	391	17	R97559
		42	811	48.7	150	21	Y51079
		43	736	44.2	173	21	Y51066
		44	731	43.9	173	21	Y51067
		45	621	37.3	146	21	Y51071
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		230					

XX This sequence represents a new purified T-cell receptor (TCR) beta-like protein (TCRLP). The TCRLPs are essential to the formation of a functional TCR and play a role in antigen recognition by T cells.  
 CC The TCRLP polypeptides and polynucleotides appear to play a role in cancer and autoimmune disorders. The TCRLP and agonists can be used for treating cancer. TCRLP antagonists can be used for treating autoimmune disorders, e.g. AIDS, Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma, atherosclerosis, bronchitis, cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis, dermatomyositis, diabetes mellitus, erythema nodosum, atrophic gastritis, glomerulonephritis, gout, Graves' disease, hyperesinophilia, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoporosis, osteoarthritis, pancreatitis, polymyositis, rheumatoid arthritis, scleroderma, Sjogren's syndrome, and autoimmune thyroiditis, complications of cancer, haemodialysis, and extracorporeal circulation, viral, bacterial, fungal, protozoal, and helminthic infections and trauma. The products can also be used for detection, diagnosis and drug screening.  
 XX Sequence 314 AA;

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC 1 MGTRLLCWAALCLGADHTGAGVQSQTESNKYTEKGKDVELDQPTISGHTAIXWYROSLLQQ 60  
 CC 1 mgtrllcwaalcilgadhtgaaqsgtqsnktrekgdvelclqpsigthaixwyrqslqq 60  
 CC XX WO9941375-A2.  
 CC FT 19-AUG-1999.  
 CC PD 19-AUG-1999.  
 CC XX 99WO-US050572.  
 CC PR 12-FEB-1998; 98US-0022939.  
 CC XX (INCY) INCYTE PHARM INC.  
 CC PI Au-Young J, Bandman O, Baughn M, Corley NC, Guegler KJ;  
 CC PI Hillman JL, Iai P, Shah P, Tang YT, Yue H;  
 CC XX DR WPI: 1999-494536/41.  
 CC DR N-PSDB: 206373.  
 CC XX New human receptor proteins, used e.g. to treat, prevent and diagnose gastrointestinal and developmental disorders - and related nucleic acids, vectors, transformed cells, antibodies, agonists and antagonists  
 CC XX PS Claim 1; Page 85-86; 94pp; English.  
 CC XX The Human receptor protein 8 (HURP-8) shares 87% identity with human T-cell receptor beta.  
 CC CC HURP-8 is expressed in cancerous, inflamed, haematopoietic/immune and gastrointestinal tissue. HURP-4 therefore appears to have a role in some forms of cancer, inflamed, haematopoietic/immune and gastrointestinal disorders.  
 CC CC This gives rise to the possibility of using an antagonist or an antibody of HURP to treat or prevent cancer or autoimmune/inflammatory disorders.  
 CC XX SQ Sequence 314 AA;  
 CC XX RESULT 2  
 CC Y15229 standard; protein; 314 AA.  
 CC XX Homo sapiens.  
 CC AC Y15229;  
 CC DT 26-OCT-1999 (first entry)  
 CC DE Human receptor protein (HURP) 8 amino acid sequence.  
 CC KW receptor; cancer; autoimmune disorder; inflammation;  
 CC KW antagonist; cell surface protein; cell signalling;  
 CC KW antibody; human receptor protein; HURP; reproductive disorder;  
 CC KW developmental disorder; gastrointestinal disorder.  
 CC OS Location/Qualifiers  
 CC Key 1 mgtrllcwaalcilgadhtgaaqsgtqsnktrekgdvelclqpsigthaixwyrqslqq 60  
 CC Misc-difference 205  
 CC /note= "Potential N-glycosylation site"  
 CC FT Db 1 mgtrllcwaalcilgadhtgaaqsgtqsnktrekgdvelclqpsigthaixwyrqslqq 60

FT Misc-difference 312  
 FT /note= "Potential cAMP/cGMP-dependent protein kinase phosphorylation site"  
 FT Misc-difference 101  
 FT /note= "Potential casein kinase II-phosphorylation site"  
 FT Misc-difference 133  
 FT /note= "Potential casein kinase III-phosphorylation site"  
 FT Misc-difference 152  
 FT /note= "Potential casein kinase III-phosphorylation site"  
 FT Misc-difference 239  
 FT /note= "Potential casein kinase III-phosphorylation site"  
 FT Misc-difference 26  
 FT /note= "Potential protein kinase C-phosphorylation site"  
 FT Misc-difference 81  
 FT /note= "Potential protein kinase C-phosphorylation site"  
 FT Misc-difference 95  
 FT /note= "Potential protein kinase C-phosphorylation site"  
 FT Misc-difference 159  
 FT /note= "Potential protein kinase C-phosphorylation site"  
 FT Misc-difference 212  
 FT /note= "Potential protein kinase C-phosphorylation site"  
 FT PN 05-FBB-1999;  
 XX 99WO-US050572.  
 XX PR 12-FEB-1998;  
 XX XX (INCY) INCYTE PHARM INC.  
 XX PI Au-Young J, Bandman O, Baughn M, Corley NC, Guegler KJ;  
 XX PI Hillman JL, Iai P, Shah P, Tang YT, Yue H;  
 XX DR WPI: 1999-494536/41.  
 XX DR N-PSDB: 206373.  
 XX PS Claim 1; Page 85-86; 94pp; English.  
 XX The Human receptor protein 8 (HURP-8) shares 87% identity with human T-cell receptor beta.  
 CC CC HURP-8 is expressed in cancerous, inflamed, haematopoietic/immune and gastrointestinal tissue. HURP-4 therefore appears to have a role in some forms of cancer, inflamed, haematopoietic/immune and gastrointestinal disorders.  
 CC CC This gives rise to the possibility of using an antagonist or an antibody of HURP to treat or prevent cancer or autoimmune/inflammatory disorders.  
 CC XX SQ Sequence 314 AA;  
 CC XX Query Match 86.1%; Score 1433; DB 20; Length 314;  
 CC CC Best Local Similarity 86.6%; Pred. No. 3.1e-123;  
 CC CC Matches 272; Conservative 12; Mismatches 30; Indels 0; Gaps 0;  
 CC CC /note= "Potential N-glycosylation site"











FT	Modified-site	76	/note= "N-glycosylation site"	Qy	295 AVLVSAVLMAMVKKRDKDSRG 314
FT	Modified-site	89	/note= "N-glycosylation site"	Db	297 avlvsaVlmamvKrkdsrg 316
FT	Modified-site	207	/note= "N-glycosylation site"	RESULT 11	
FT	XX	WO200008155-A2.		Y51069	
PN	XX			ID Y51069 standard; protein; 179 AA.	
PD	17-FEB-2000.			XX	
XX				AC Y51069;	
PF	06-AUG-1999;	99W0-US17777.		XX	
XX	07-AUG-1998;	98US-0160065.		DT 22-MAR-2000 (first entry)	
PR	01-SEP-1998;	98US-0098703.		XX	
XX				DE Human TCRbeta protein fragment #2.	
PA	( INCY - ) INCYTE PHARM INC.			KW T cell receptor beta; TCRbeta; human; constant region;	
XX				KW immunosuppressor.	
PI	Hillman JL, Yue H, Lai P, Tang YT, Gorgone GA, Guegler KJ;			XX	
PI	Corley NC, Baugn MR;			OS Homo sapiens.	
XX				XX	
DR	WPI: 2000-205710/18.			JP11302299-A.	
DR	N-PSDB; Z50901.			XX	
XX				PN 02-NOV-1999.	
XX				XX	
PT	New human receptor-associated proteins (HRAP) useful for the diagnosis, treatment and prevention of cell proliferative, autoimmune, inflammatory, reproductive, cardiovascular, and gastrointestinal disorders			XX	
PT				XX	
PS	Claim 1: Page 86; 9pp; English.			XX	
XX	The present sequence is a human receptor-associated protein (HRAP) from Incyte clone 2656082 obtained from THYMNOT04 cDNA library.			XX	
CC	This sequence is expressed in haematopoietic/immune, gastrointestinal and reproductive tissues. HRAP has cytosstatic, immunomodulatory, antiinflammatory, cardiotonic, antiarteriosclerotic, hepatotropic, CC antiasthmatic, antidiabetic, dermatological, antiallergic, antianæmic, CC activities. The present sequence is useful in the diagnosis, treatment CC and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory, reproductive, CC cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, CC cirrhosis, leukaemia, cancer, AIDS, arthritis, anaemia, CC asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and CC irritable bowel syndrome).			XX	
XX				XX	
Sequence	316 AA;			XX	
SQ				XX	
Query Match	71.0%	Score 1182; DB 21; Length 316;		XX	
Best Local Similarity	74.1%	Pred. No. 2.8e-100; Mismatches 18; Indels 10; Gaps 3;		XX	
Matches	237	Conservative		XX	
Qy	1 MGTRLCWAALCLLGADHTGAGVSQTSPLNSRKYTKGSKDVEILRCDPISGHATAWYRQSLGQ 60			XX	
Db	1 mgcrllicavcllgavpmegvtqgtprhvmgmtnkkslkceghlgnamwykqsakk 60			XX	
Qy	61 GPEFLIYFGTGAADDGSLPNDFFAVRPEGSVSTLKIORTEGDSAAAYRA-----GV 114			XX	
Db	61 plelmfvysleervennvspsrfspecpnshflhltlqpedasylcassvhpgd 119			XX	
Qy	115 AGGWSSYEQFGPCGRILTVLEDLKNVFPPEVAYEPSEBEISHTOKARLYCILATGFYFD 174			XX	
Db	120 argg---ineqfqfpgrtritiedlnkvfppeavfpeaseeishtqkatlvclatgfypd 176			XX	
Qy	175 FWELSMWNNGKEVHSGVYSTDQPQKPALNDRCVLSRSLRVSATFWONPRHFRQVQ 234			XX	
Db	177 fwelsmwnngkevhsystdpqpqlkeqpalndrcvlsrslrvsatfwonprhfrcqvg 236			XX	
Qy	235 FYGLSENDEWTQDRAKPVQIVSABA WGRADCGFTSESYQGVLSATIYEILLGKATLY 294			XX	
Db	237 fyglsendewtqdrakpvqivsaaawgradcgftsesyqgvlsatilyeillgkatiy 295			XX	
RESULT	12			XX	
Y05j03				XX	
ID	Y05j03 standard; protein; 303 AA.			XX	
AC	Y05j03;			XX	
DE	02-JUL-1999 (first entry)			XX	

DE Killer T-cell receptor protein sequence.  
 XX  
 KW Killer T-cell receptor; HIV; infection; HIV-1 IIIB; therapy.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9916885-A1.  
 XX  
 PD 08-APR-1999.  
 XX  
 PF 28-SEP-1998; 98WO-JP04 345.  
 XX  
 PR 26-SEP-1997; 97JP-0262336.  
 XX  
 PA (KYOWA ) KYOWA HAKKO KOGYO KK.  
 PA (SAIT/ ) SAITO T.  
 PA (TAKA/ ) TAKAHASHI H.  
 XX  
 PI Saito T, Takahashi H;  
 XX  
 DR WPI: 1999-255096/21.  
 DR N-PSDB; X36391.  
 XX  
 PT Killer T-cell receptor peptide specifically recognizing HIV-infected  
 PT cells  
 XX  
 PS Claim 7; Page 60-62; 75pp; Japanese.  
 PS This sequence is a killer T-cell receptor protein of the invention,  
 XXX which recognises and damages cells infected with human immunodeficiency  
 CC virus (HIV), especially with HIV-1 IIIB. The receptor can be used as  
 CC a constituent of compositions for the treatment of HIV infection.  
 CC  
 SQ Sequence 303 AA;

	Query Match	Score	DB 20:	Length	303;
Best Local Similarity	55.6%	Score	925.5,	DB 20:	Length 303;
Matches 188; Conservative	60.3 %;	Pred.	No. 7.6e-77;		
Matches 188; Mismatches	34;	Mismatches	81;	Indels	9;
				Gaps	4;
Qy	1 MGTRILCWAIICLLGADHTGGAGVSQPSNSKTYTERGKADVEILRDPISCHTALWYRSGLQ	60			
Db	1 mgstrlf-fvvllicakhmeaaatgspksrvatggktvlschqtnhdnywyrqdtgh	59			
Qy	61 GPEFLITYFGQGAADDGLPNDREFAVRPBESSVSTURKIQREQGDSSAYLRGVAAWS	120			
Db	60 g1rlhyssyadstekgkdp dgyksrspsgenfsilelaslsqavf ---cassegr	115			
Qy	121 YNEQYFQGPTRLVLEDLNKVNPPEVAVFESEAEISHTQATLYCLATGFYPDHBLSW	180			
Db	116 eaqffgpptrlvledlnvtppkyslfpesklaenkqatlvclargffpdhvlsw	175			
Qy	181 WNGKEVHSGSYSTDPOPPLKEOPALNDSYCLSSRRVSYATFWONPRNHFRCOYFGLE	240			
Db	176 wngtvehsgystdpopake ---syscyslrlsvsatfwnprfrcoyfgle	231			
Qy	241 NDEWTQDRAKPTVOTYSAEANGRADCGFTSESYQCGVLSATIYEUILGKATLYAVLYSA	300			
Db	232 edkwpgspkptqnsaevgradgeitsasyhggvisatyleuilgkatiyavysg	291			
Qy	301 IYLMAMVKRKDS	312			
Db	292 ivlmamvkkn3	303			
	RESULT	13			
Y51068	ID	Y51068	standard;	protein;	177 AA.
XX	AC	Y51068;			
XX	DT	22-MRD-2000	(55nt)		

Human TCRbeta protein fragment #1.  
T cell receptor beta; TCRbeta; human; constant region;  
immunosuppressor.

Homo sapiens.

JP1102299-A.  
02-NOV-1999.  
21-APR-1998; 98JP-0110607.  
21-APR-1998; 98JP-0110607.  
(KIRIN ) KIRIN BREWERY KK.  
WPI; 2000-075345/07.

T cell receptor beta chain constant region peptide - h  
immunosuppressing activity

Disclosure; Page 11; 15pp; Japanese.

This invention describes a novel polypeptide comprising  
part or all of the constant region of T cell receptor  
(TCRbeta) and containing substantially no other region  
having immunosuppressing activity. The TCRbeta require  
of tissue-compatible antigen for the patient to be dos-  
specificity. This sequence represents a fragment of the  
protein described in the method of the invention.

Sequence 177 AA;

Query Match	54.5%	Score	907	DB	21;	Length	177;
Best Local Similarity	97.7%	Pred.	No.	1.8e-75;			
Matches	172;	Conservative	1;	Mismatches	3;	Indels	0;
Qy	136	EDLKNVPPPEAVFEPSEAEISHTOKATLVLCLATGFYDPIHVELSWNVNGEVEHSGYSTDP	195				
Db	1	edlnkvpppeavfepseaeishtqatlvclatgfypdihvelswnvngvehsjvstdp	60				
Qy	196	QPLKEQPALNDSCRYCSSLSSRLRVSATWQNPRNHFRCQVQFYQLSENDEWTKODRAKPVTOI	255				
Db	61	qplkeqpaldnsrycsslssrlrvsatwqnprnfhrcqvfqylsendsewcqdrakpvtki	120				
Qy	256	VSAEAANGRADCGFTSETSYQQGVLSATIYLIELLGRATLYAVLVSALVLMANVKRKD	311				
Db	121	vseaangradcgftsvyqqgvlsatilyeilgklatlyavlsalvlmamvkrd	176				
RESULT	14						
P50252							
ID	P50252	standard; Protein:	306 AA.				
XX							
P50252;							
AC							
XX							
DT	07-OCT-1991	(first entry)					
XX							
DE	Sequence of T-cell antigen receptor beta chain encoded by cDNA						
DE	clone 86T1.						
XX							
KW	Diagnosis; site-directed therapy.						
XX							
OS	Hom sapiens.						
XX							
FH		Location/Qualifiers					
FT	Key peptide	1..19					
FT		/label= leader					
FT		20..117					
Region		/label= variable					
FT		21..120					
FT		/label= variable					



Qy 3 TRILCHAAALCLIGADHTGAGYSQTPSNKVPTEKGKDVELRCDPISGHTALWYROSILGGQP 62  
 Db 13 tellisvalfillgtkmeavtqsprnkavtggtvilsenqtanhnnnwywrdtgngl 72  
 Qy 63 EFLIIHQGTGAADDSELPLNDRFAVRPREGYSTLTKQRREQDSDAYLRAQVARGWSSIN 122  
 :  
 Db 73 zlihyssgagstekekdp-agykastpsqensfslllelatpsqtsvycasqdgqlgs-e 130  
 Qy 123 EGYFGPDTTRUVLDELDKVNFPPEAVFEPSEAEIHTQKATLYCLETATGFYPDHVELSWVV 182  
 :  
 Db 131 tlyfgstrityledrnrvpkvsfepkraeinlkqatlvclargffpdhvlsww 190  
 Qy 183 NGKEVHSGVSTDQPLIKEQPAALNDSRYCYLSRRLVYSATEFWONPRNHRFCOQFYGLSEND 242  
 :  
 Db 191 ngkevhsgvstdcpayke---snscyclsrlysatfwhnprhfrccqfqglseed 246  
 Qy 243 FWTQDRAKPYNTQIVSAEAANGRADCGFTSESYQQGYLSATTIYEILGKATLYAVLYSALV 302  
 :  
 Db 247 hwpesgspkpvir-tsvarpgaeqcgits-syhggvisatilyeiliqkatlyavysgv 304  
 Qy 303 LMAMVKRKDS 312  
 :  
 Db 305 lmamvkkns 314

Search completed: October 11, 2000, 06:08:36  
 Job time: 30 sec

This page is part of USpto

GenCore version 4.5  
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OM protein - protein search, using sw model  
Run on: October 11, 2000, 06:08:11 ; Search time 12.56 Seconds  
(without alignments)  
419,030 Million cell updates/sec

Title: US-09-405-940-1  
Perfect score: 1664  
Sequence: 1 MOTRLLCWAALCLLGADHTG.....AVLYSALVLMAMVKRKDSRG 314

Scoring table: BLOSUM62  
Gappen: 10.0 , Gapext: 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:  
 3: /cgn2\_5/ptodata/1/iaa/6\_COMB.pep:  
 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:  
 5: /cgn2\_6/ptodata/1/iaa/backfile1.pep:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Length	DB ID	Description
1	1664	100.0	314	3 US-09-897-097-1	Sequence 1, Appli
2	1394.5	83.8	311	3 US-08-897-097-3	Sequence 3, Appli
3	1132	80.0	310	3 US-08-897-097-4	Sequence 4, Appli
4	895	53.8	314	5 541340	Patent No. 541340
5	868.5	52.2	293	5 5189147	Patent No. 5189147
6	827	49.7	391	4 PCM-US95-15696-2	Sequence 2, Appli
7	707	42.5	266	5 5115384	Patent No. 5115384
8	584.5	35.1	217	5 5189147-7	Patent No. 5189147
9	265	15.9	102	3 US-08-466-368-9	Sequence 9, Appli
10	243.5	14.6	236	3 US-08-477-550-10	Sequence 10, Appli
11	239	14.4	234	3 US-08-487-550-2	Sequence 2, Appli
12	237	14.2	235	2 US-08-378-939-12	Sequence 12, Appli
13	236.5	14.2	235	2 US-08-400-753-8	Sequence 8, Appli
14	228.5	13.7	213	3 US-08-600-820-6	Sequence 6, Appli
15	224	13.5	241	2 US-07-936-098A-56	Sequence 56, Appli
16	222.5	13.4	232	1 US-08-704-744-80	Sequence 80, Appli
17	222.5	13.4	239	3 US-08-487-550-6	Sequence 6, Appli
18	220.5	13.3	214	1 US-08-438-516-12	Sequence 12, Appli
19	220.5	13.3	274	1 US-08-266-966A-19	Sequence 19, Appli
20	219	13.2	242	1 US-08-398-61A-56	Sequence 56, Appli
21	219	13.2	242	1 US-08-398-612A-56	Sequence 56, Appli
22	219	13.2	242	1 US-08-398-611A-56	Sequence 56, Appli
23	219	13.2	242	2 US-08-491-330A-56	Sequence 56, Appli
24	219	13.2	242	3 US-09-024-449-42	Sequence 42, Appli
25	219	13.2	242	3 US-08-804-444A-42	Sequence 42, Appli
26	216.5	13.0	218	2 US-08-897-355B-15	Sequence 15, Appli
27	216.5	13.0	218	2 US-08-887-355B-17	Sequence 17, Appli
28	216.5	13.0	218	2 US-08-887-352B-19	Sequence 19, Appli

Query Match 83.8%; Score 1394.5%; DB 3; Length 311;  
 Best Local Similarity 85.4%; Pred. No. 6.3e-141;  
 Matches 268; Conservative 14; Missmatches 3; Gaps 2;

Qy	1	MGTRLICWAALLGADHTAGSOTPSNKVTKVGDYLRCDFISGHLYWRSQIQQ 60
Db	1	MGTRUICWAALLGADHTAGSOTPSNKVTKVGDYLRCDFISGHLYWRSQIQQ 60
Qy	61	GPEFLYFGPGRTRLVDELDLKVNFPPEVAVEPSEAEISHQKATLVCLATGFYDPDHVELSW 120
Db	61	GPEFLYFGTGAADSGLPNDREFAVRPGSVSTKLKORTEDSAAYLRAGVAAGWSS 120
Qy	121	YNEQYFGPGRTRLVDELDLKVNFPPEVAVEPSEAEISHQKATLVCLATGFYDPDHVELSW 180
Db	121	YNEQYFGPGRTRLVDELDLKVNFPPEVAVEPSEAEISHQKATLVCLATGFYDPDHVELSW 180
Qy	181	WNGKEVHSVSYSTDQPKLQEPAQALNSRCVLSLRSVATEWQNPRNHRFCQVFYGLSE 240
Db	181	WNGKEVHSVSYSTDQPKLQEPAQALNSRCVLSLRSVATEWQNPRNHRFCQVFYGLSE 240
Qy	241	NDEWTQDRAKPTQIVSAWGRADCGFTSESYQQGVLSATILYELIGKATLYAVLYSA 300
Db	241	NDEWTQDRAKPTQIVSAWGRADCGFTSESYQQGVLSATILYELIGKATLYAVLYSA 300
Qy	301	LVLMMAMVKRDSSRG 314
Db	301	LVLMMAMVKRDSSRG 314
RESULT 2		
		; Sequence 3, Application US/08897097
		; Patent No. 6054292
		GENERAL INFORMATION:
		APPLICANT: Hillman, Jennifer L.
		TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
		NUMBER OF SEQUENCES: 4
		CORRESPONDENCE ADDRESS:
		ADDRESSEE: Incyte Pharmaceuticals, Inc.
		STREET: 3174 Porter Drive
		CITY: Palo Alto
		STATE: CA
		COUNTRY: USA
		ZIP: 94304
		COMPUTER READABLE FORM:
		MEDIUM TYPE: Diskette
		COMPUTER: IBM Compatible
		OPERATING SYSTEM: DOS
		SOFTWARE: FastSeq for Windows Version 2.0
		CURRENT APPLICATION DATA:
		APPLICATION NUMBER: US/08/897,097
		FILING DATE: Herewith
		CLASSIFICATION: 536
		PRIOR APPLICATION DATA:
		APPLICATION NUMBER:
		FILING DATE:
		ATTORNEY/AGENT INFORMATION:
		NAME: Billings, Lucy J.
		REGISTRATION NUMBER: 36,749
		TELECOMMUNICATION INFORMATION:
		TELEPHONE: 415-855-0555
		TELEFAX: 415-845-4166
		TELEX:
		INFORMATION FOR SEQ ID NO: 3:
		SEQUENCE CHARACTERISTICS:
		LENGTH: 310 amino acids
		TYPE: amino acid
		STRANDEDNESS: single
		TOPOLOGY: linear
		IMMEDIATE SOURCE:
		LIBRARY: GenBank
		CLOSE: 1100182
		US -08-897-097-3

RESULT 3

US-08-897-097-4		
		; Sequence 4, Application US/08897097
		; Patent No. 6054292
		GENERAL INFORMATION:
		APPLICANT: Hillman, Jennifer L.
		APPLICANT: Corley, Neil C.
		TITLE OF INVENTION: T-CELL RECEPTOR BETA-LIKE PROTEIN
		NUMBER OF SEQUENCES: 4
		CORRESPONDENCE ADDRESS:
		ADDRESSEE: Incyte Pharmaceuticals, Inc.
		STREET: 3174 Porter Drive
		CITY: Palo Alto
		STATE: CA
		COUNTRY: USA
		ZIP: 94304
		COMPUTER READABLE FORM:
		MEDIUM TYPE: Diskette
		COMPUTER: IBM Compatible
		OPERATING SYSTEM: DOS
		SOFTWARE: FastSeq for Windows Version 2.0
		CURRENT APPLICATION DATA:
		APPLICATION NUMBER: US/08/897,097
		FILING DATE: Herewith
		CLASSIFICATION: 536
		PRIOR APPLICATION DATA:
		APPLICATION NUMBER:
		FILING DATE:
		ATTORNEY/AGENT INFORMATION:
		NAME: Billings, Lucy J.
		REGISTRATION NUMBER: 36,749
		TELECOMMUNICATION INFORMATION:
		TELEPHONE: 415-855-0555
		TELEFAX: 415-845-4166
		TELEX:
		INFORMATION FOR SEQ ID NO: 4:
		SEQUENCE CHARACTERISTICS:
		LENGTH: 310 amino acids
		TYPE: amino acid
		STRANDEDNESS: single
		TOPOLOGY: linear
		TMEDIATE SOURCE:
		LIBRARY: GenBank
		CLOSE: 1100182
		US -08-897-097-3

LIBRARY: GenBank  
 CLONE: 339012  
 3-08-897-097-4

Query Match Score 80.0%; Best Local Similarity 81.7%; Pred. No. 3e-134; Matches 254; Conservative 17; Mismatches 38; Indels 2; Gaps 1;

1 MSTRLLCAACLLGADHTGAGVSQTPSNKTYEKGDVLERCDPISGHTALYWRSLGQ 60  
 1 MGTSLCWMACLLGADHTGAGVSQTPSNKTYEKGDVLERCDPISGHTALYWRSLGQ 60

61 GPEFLYFQGTGAADSGLIPDRFAVPEGSVSTIKQTDEQGDSAAIYDRAGYAAGWS 120  
 61 GPEFLYFQNEAQLERSRLSDRFESLRPKGSFSTILEQTDEQGDSAMYLCASSLGLN 119

61 GPEFLYFQNEAQLERSRLSDRFESLRPKGSFSTILEQTDEQGDSAMYLCASSLGLN 119

121 YNEQYFQGPTRILLEDLKNYFPEVAVPEPEAVFSEAEIHTIQATLYCLATGFYDPDHVELSW 180  
 120 -QPOHSGDTRSLTILEDLNKYFPEVAVPEPEAVFSEAEIHTIQATLYCLATGFYDPDHVELSW 178

181 WNGKEYVHSYSTDPOPLKEQPALNDSRYCFSRSLRVSAFWQNPNHFRFCQVQFYGLSE 240  
 179 WNGKEYVHSYSTDPOPLKEQPALNDSRYCFSRSLRVSAFWQNPNHFRFCQVQFYGLSE 238

241 NDEWTQDRAKPTQIVSAEAWGRADGFTSESYQQGVLSATIYLEILLGKATLYAVLVSA 300  
 239 NDEWTQDRAKPTQIVSAEAWGRADGFTSESYQQGVLSATIYLEILLGKATMYAVLVSA 298

301 LVLMANKRKD 311  
 299 LVLMANKRKD 309

RESULT : 4

Patent No. 543440  
 APPLICANT: KRIMPFENFORT, PAULUS J.-A.; BURNS, ANTONIUS J.M.  
 TITLE OF INVENTION: TRANSGENIC MICE DEPLETED IN MATURE  
 -CELLS AND METHODS FOR MAKING TRANSGENIC MICE  
 NUMBER OF SEQUENCES: 7  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 07/919,936  
 FILING DATE: 27-JUL-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 280,218  
 FILING DATE: 05-DEC-1988  
 SEQ ID NO:7  
 LENGTH: 314  
 34340-7

Query Match Score 80.0%; Best Local Similarity 81.7%; Pred. No. 3e-134; Matches 182; Conservative 34; Mismatches 86; Indels 8; Gaps 3;

13 TTLISWALFLIGTKMHEAVTQSPPANKVAVTGGKVTLSNQTNHHNMCYRADGHTL 72  
 3 TRLLCAACLLGADHTGAGVSQTPSNKTYEKGDVLERCDPISGHTALYWRSLGQGP 62

63 EFLYFQGTGAADSGLIPDRFAVPEGSVSTIKQTDEQGDSAAIYDRAGYAAGWSYN 122  
 73 RLIHYSGLGSTEKGDP-DQYKPSPSQEDPSLTLAPSQTSYF--CASSDNSE 128

123 EQYFGDGTRSLTILEDLKNYFPEVAVPEPEAVFSEAEIHTIQATGFYDPDHVELSWWV 182  
 129 TLYFGSOTRSLTILEDLKNYFPEVAVPEPEAVFSEAEIHTIQATGFYDPDHVELSWWV 188

183 NGKEYVHSYSTDPOPLKEQPALNDSRYCFSRSLRVSAFWQNPNHFRFCQVQFYGLSE 242  
 189 NGKEYVHSYSTXQPAKE---SNYSYCLSSRLRVSAFWHNPNHFRFCQVQFHGLSEEK 244

243 BWTDQDRAKPTQIVSAEAWGRADGFTSESYQQGVLSATIYLEILLGKATLYAVLVSAVY 302

RESULT : 5

Patent No. 5189147  
 APPLICANT: SAITO, HARUO; KRAHNZ, DAVID M.; ELSEN, HERMAN N.;  
 TITLE OF INVENTION: METERODIMERIC T LYMPHOCYTE RECEPTOR  
 ; ANTIBODY  
 NUMBER OF SEQUENCES: 21  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 07/271,216  
 FILING DATE: 14-NOV-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 666, 988  
 FILING DATE: 31-OCT-1984  
 APPLICATION NUMBER: 620,122  
 FILING DATE: 13-JUN-1984  
 SEQ ID NO:7  
 LENGTH: 293  
 5189147-3

Query Match Score 52.2%; Best Local Similarity 57.9%; Pred. No. 9 4e-85; Matches 175; Conservative 34; Mismatches 82; Indels 11; Gaps

Qy 11 LCLIGADHTGAGVSQTPSNKTYEKGDVLERCDPISGHTALYWRSLGQPEFLYFQG 70  
 Db 3 LCFLGTLVLDVKVTONRSYLLKRMGNVNLBCGQDMSHETMYWDPGLGQLQIYSD 62

Qy 71 TGAADDSGLPNDRFFAVPREGSVSTIKQTDEQGDSAAIYDRAGYAAGWSYNQYFGPT 130  
 Db 63 VDSNSSGDIPKG-YRYSRKKREHESLIDSATKNTQNSVYTCAGGAP----EQYFGPT 115

Qy 131 RLTIVEDLKNVEPPEAVFSEAEIHTIQATLYCLATGFYDPDHVELSWWVNGKEVHSG 190  
 Db 116 RLTIVEDLNRNTPPKSFLFEESKAENKOKATLYCLARGEPPDHVELSWVNGREVEHSG 175

Qy 191 VSTDPOPLKEQPALNDSRYCFSRSLRVSAFWQNPNHFRFCQVQFHGLSEEDKWPSPK 250  
 Db 176 VSTDPOPLKEQPALNDSRYCFSRSLRVSAFWHNPNHFRFCQVQFHGLSEEDKWPSPK 231

Qy 251 PVTQIVSAEAWGRADGFTSESYQQGVLSATIYLEILLGKATLYAVLVSAVLMAMVKK 310  
 Db 232 PVTQNSAEMGRADGFTSESYQQGVLSATIYLEILLGKATLYAVLVSGVLVLMAMVKK 291

RESULT : 6

PCT-US95-15696-2  
 Sequence 2, Application PC/TUS95-15696  
 GENERAL INFORMATION:  
 APPLICANT: President and Fellows of Harvard College  
 TITLE OF INVENTION: SINGLE CHAIN T-CELL RECEPTOR  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kevin M. Farrell, P.C.  
 STREET: P.O. Box 999  
 CITY: York Harbor  
 STATE: Maine  
 COUNTRY: USA  
 ZIP: 03911  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patientin Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/156965  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY/AGENT INFORMATION:  
 NAME: Farrell, Kevin M.  
 REFERENCE/DOCKET NUMBER: 35, 505  
 FILING DATE: 06-DEC-1994  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 207-363-0558  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 391 amino acids  
 TYPE: amino acid  
 MOLECULE TYPE: linear  
 PCT/US95/15696-2

Query Match 49.7%; Score 827; DB 4; Length 391;  
 Best Local Similarity 62.9%; Pred. No. 4e-80;  
 Matches 168; Conservative 17; Mismatches 30; Indels 52; Gaps 6;

Qy 15 GADHTGAGYSQTSPSNKVTKEKGDKVELRCDPISGHITALWYRQLGQQPEFLYFQFTGAA 74  
 Db 150 GSD-EDG-GT-QSPAYLFKEQGNVNTLSCEQNLNHDAMYWRQDPGQGIR-LIYY----- 201  
 Qy 75 DSGGLPNDRFPAVRFPEGSVSTLKTQRTFQGDASAYLRAGVAWS----- 119  
 Db 202 -SEIVND-----FQKGD-----TAGSYSREKKESFPLTVTS 233

Qy 120 -SYNQYFGPGTRTFLDKNVPEPVEAEPSEAEISHTOKATLVCLATGFYFPDIVE1 178  
 Db 234 AOKNPTAFEGPNRNLTVLEDKNVPEPVEAEPSEAEISHTOKATLVCLATIFPDHEVL 293

Qy 179 SWWNGKEYHSGYSTDPOPLKEOPALNDSRYCCLSSRLRVSAFEWQNPRNHFRCQOYFGL 238  
 Db 294 SWWNGKEYHSGYSTDPOPKHEOPALNDSRYCCLSSRLRVSAFEWQNPRNHFRCQOYFGL 353

Qy 239 SENDWTQDRAKPVTCQIVSAEANGRAD 265  
 Db 354 SENDWTQDRAKPVTCQIVSAEANGRAD 380

RESULT 7  
 SEQ ID: 11; FILING DATE: 5-DEC-1988  
 LENGTH: 266

Query Match 42.5%; Score 707; DB 5; Length 266;  
 Best Local Similarity 54.2%; Pred. No. 1.5e-67;  
 Matches 142; Conservative 32; Mismatches 80; Indels 8; Gaps 3;

Qy 3 TRLLCWAACLIGADHTGAGVSOTPSNKVTKEKGDKVELRCDPISGHITALWYRQLGQQP 62

---

Db 13 TTLSSWVALFULLGKHEMAVQTSPRKAVTGGKVTLSCNOTINHNHNNCYRADTGTL 72  
 Qy 63 EFLIYFQGTAQDSSLPLNDRFAVRFPEGSVSTLKTQRTFQGDASAYLRAGVAWS 122  
 Db 73 RLIHYSGLGSLIEKGDIIP-DGYKPSRPSQDFDSLLELATPSQTSVYF--CASGDNSE 128  
 Qy 123 EQYFGFGRTRTFLDKNVPEPVEAEPSEAEISHTOKATLVCLATGFYFPDIVE1 182  
 Db 129 TLYFGSGTRTFLDILRNTPPKVSLFEPSKAEIANKQATLVCLARGFYFPXHVYLSEND 188  
 Qy 183 NGKEVHSGVSTDPOPLKEOPALNDSRYCCLSSRLRVSAFEWQNPRNHFRCQOYFGLSEND 242  
 Db 189 NGKEVHSGVSTDPOPLKEOPALNDSRYCCLSSRLRVSAFEWQNPRNHFRCQOYFGLSEND 244  
 Db 245 KWPEGSKPVQTQPAKE---SNYSYCLSSRLRVSAFEWQNPRNHFRCQOYFGLSEND 266

RESULT 8  
 SEQ ID: 7  
 FILING DATE: 05-DEC-1988  
 LENGTH: 217;  
 ; Patent No. 5189147  
 ; APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; ELSEN, HERMAN N.;  
 ; TONEAWA, SUSUMU  
 ; TITLE OF INVENTION: METEROIDIMERIC T LYMPHOCYTE RECEPTOR  
 ; ANTI BODY  
 ; NUMBER OF SEQUENCES: 21  
 ; CURRENT APPLICATION DATA:  
 ; Application Number: US/07/271,216  
 ; Filing Date: 14-NOV-1988  
 ; Prior Application Data:  
 ; Application Number: 666,988  
 ; Filing Date: 31-OCT-1984  
 ; Application Number: 620,122  
 ; Filing Date: 13-JUN-1984  
 ; Seq Id No.: 7;  
 ; Length: 217  
 5189147-7

Query Match 35.1%; Score 584; DB 5; Length 217;  
 Best Local Similarity 51.8%; Pred. No. 1.3e-54;  
 Matches 116; Conservative 31; Mismatches 66; Indels 11; Gaps 3;

Qy 23 VSQTPSNKVTKEKGDKVELRCDPISGHITALWYRQLGQQPEFLYFQGTGAADDGELPND 82  
 Db 4 VTQMSRYLIKMGGENVLLCQDMHHEIMWYRQDPGLQQLIVTSDNSGDIKRG 63  
 Qy 83 RFFAVRFPEGSVSTLKTQRTFQGDASAYLRAGVAWSNEQYKGPGRNLTVLEDLKNYF 142  
 Db 64 -YRVSRKKREHFSLILDSAKTNOTSVFQCGAP----EQYFGPQTIVLTVLEDLRLNVT 116

Qy 143 PPEVAEPSEAEISHTOKATLVCLATGFYFPDHVLSWQNGKEVHSGVSTDPPPLKECP 202  
 Db 117 PPKVSLFEPSEAEISHTOKATLVCLARGFYFPDHVLSWQNGREHSGVSTDPPPLKECP 202

Qy 203 ALNDSYCLSSRLRVSAFEWQNPRNHFRCQOYFGLSENDWTQ 246  
 Db 175 -SNYSYCLSSRLRVSAFEWQNPRNHFRCQOYFGLSENDWTQ 216

RESULT 9  
 SEQ ID: 11; FILING DATE: 5-DEC-1988  
 LENGTH: 266

Sequence 9, Application US/08466338  
 ; Patent No. 603539  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maddon, Paul J.  
 ; APPLICANT: Littman, Dan R.  
 ; APPLICANT: Chess, Leonard  
 ; APPLICANT: Axel, Richard  
 ; APPLICANT: Weiss, Robin  
 ; APPLICANT: McDougal, J. S.





Best Local Similarity 31.6%; Pred. No. 2e-17; Matches 81; Conservative 36; Mismatches 88; Indels 51; Gaps 15;

Qy 21 AGYSQTPSMKVTEKGDKYVELRCDPISGHT-AIYWIYROSLSLGCGPEFLIVFGQTGAADDSG 78  
Db 1 AELTQSPGTLSLSPGERATLSCRASOGSYSLAWYQOKAGQAAPRLIYGASRRA---TG 57

Qy 79 LPNDRFFAVERPEGVSTKLRIQRTGEQDSAAYLRAQVAAGWSSYNEQY-----FPGTR 131  
Db 56 IP-DRTG-SGSQDFTLTTRLEPEDAVY-----YCQQYGSQOFETFGPGTK 104

Qy 132 LTVLEDLK-NVFPEPVEAVFEPSEAEISHTQKATLVCLATGFYDPDHVELSWNYNGKEYHSG 190  
Db 105 V---DLKTAAPSVFIFPPSDQLK-SGTASVCLNNFVPREAKVQWVYD-NALQSG 158

Qy 191 VSTDQPLKEQPALNDSYCLSSLRRLYSATFWQNPRNHFRCQYQFYGLSENDEWTQDRAK 250  
Db 159 NS---QESVTEQDS-KDSTYSLSSTLTSKADYBK-HKRYACEVTHQGLS-----S 204

Qy 251 PVTQIVSAARGRADC 266  
Db 205 PVT-----KSFNRESEC 215

RESULT 14  
US-08-630-820-6  
Sequence 6; Application US/08630820  
Patent No. 6008033

GENERAL INFORMATION:  
APPLICANT: OPPER, Martin  
APPLICANT: BOSSLER, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CRYPTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
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REGISTRATION NUMBER: 33,603  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
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TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Query Match 13.7%; Score 228, 5; DB 3; Length 213;  
Best Local Similarity 29.9%; Pred. No. 1.4e-16;

Matches 73; Conservative 42; Mismatches 94; Indels 35; Gaps 12;

Qy 23 VSQTPSNKVTEKGDKYVELRCDPISGHTALWYRQSLGQQGPFLIVEQGTGAADDSGLPND 82  
Db 5 MTQSPSSLSAVGDRVTITCSTSSVSYMHYQKPGKAKLITISTSNL---SGVPSR 61

Qy 83 REFAVREPGSVSTLKIORTGEQDSAAYLRAQVAAGWSSYNEQYFPGTRTIVLEDLKNF 142  
Db 62 -FSGSGTIDFTFISLQPEDIATY---YCHQNSY - PTFQGQTK --VEIKRTVA 110

Qy 143 PPEAVAPEPSEAEISHTQKATLVCLATGFYDPDHVELSWNYNGKEYHSGVSTDPQILKEQP 202  
Db 111 APSVFIFFPSDQLK-SGTASVCLNNFVPREAKVQWVYD-NALQSGNS---QESVTEQD 166

Qy 203 ALNDSRYCLSSRLYSATFWQNPRNHFRCQYQFYGLSENDEWTQDRAKPTQIVSAEANG 262  
Db 167 S-KDSTYSLSSSLTTSKADYBK-HKRYACEVTHQGLS-----SPVT-----KSFN 209

Qy 263 RADC 266  
Db 210 RGEc 213

RESULT 15  
US-07-916-098A-56  
Sequence 56; Application US/07916098A  
Patent No. 5871732

GENERAL INFORMATION:  
APPLICANT: BURKLY, LINDA C.  
APPLICANT: CHISHOLM, PATRICIA L.  
APPLICANT: THOMAS, DAVID W.  
APPLICANT: ROSA, DAVID R.  
APPLICANT: ROSA, JOSEPH J.  
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
TREATMENT OF AIDS, ARC AND HIV INFECTION  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
STREET: 10 SOUTH WACKER DRIVE  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: U.S.A.  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/916,098A  
FILING DATE: July 24, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/08843  
FILING DATE: NC 5871732ember 27, 1991  
CLASSIFICATION: 424  
APPLICATION NUMBER: 07/618,542  
FILING DATE: NO. 5871732ember 27, 1990  
CLASSIFICATION: 424  
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TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 241 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
MOLECULE TYPE: protein

US-07-916-098A-56

	Query Match	Score 224; DB 2; Length 241;
	Best Local Similarity	13.5%; Pred. No. 5.2e-16;
	Matches 77; Conservative	29.8%; Mismatches 41; Indels 56; Gaps 15;
Qy	23 VSQTPSNKWTGKDVELRCDPISGHITALY- - - - -	WYROSILGGPPEFLIYFQGTGA 73
Db	26 MTQSPDSLAVSLGERATINCK- SSGSLLYSFNQKNYLAWYQOKPGOPPKLILYWAST--	81
Qy	74 ADDGLPNDRFAVRPEGSVSTLKIQRTEQGGSAAAYDRAGVAGWSSYYNEQW-----	-FGP 128
Db	82 -RESGP-DR-FSGSGSGSTDFTLTISSIQAEDEVAY-----	-YCQQYSSYRTFGR 127
Qy	129 GTRUTVLEDLKNYPPEVAVEPESEAELSHTOKATLVCLATEGYPDHIVELSWNGREHV 1.88	
Db	128 GTK---LEIKRTAAAPSVFIFPSDEQLK-SGTASVCLNNFYREAKVQMKVD-NALQ 1.82	
Qy	189 SGVSTDPOPLKEPALANDSRYCLSSRLRVSAFWONPRNHFRCQVOFYGLSENDENTQDR 2.48	
Db	183 SGNS -QESVTEQDS-KDSTYSLSTLSKADYEK-HKVYACEVHQGLS -----	229
Qy	249 AKPVQTQIVSAEANGRADC 2.66	
Db	230 -SPVT-----KSFRGEC 24.1	

Search completed: October 11, 2000, 06:09:50  
 Job time: 99 sec